

SEARCH REQUEST FORM

6-518

Requestor's Name: VANDERVEGT Serial Number: 09/027,777
Date: 6/14/99 Phone: 305-6997 Art Unit: 1644
9E03

Search Topic:

Please write a detailed statement of search topic. Describe specifically as possible the subject matter to be searched. Define any terms that may have a special meaning. Give examples or relevant citations, authors, keywords, etc., if known. For sequences, please attach a copy of the sequence. You may include a copy of the broadest and/or most relevant claim(s).

PLEASE PERFORM A RUSH ~~INTERFERENCE~~ ^{REMOVED/SEE EX. REC} AND
DATABASE SEARCH OF SEQ ID NOS

1,
2,
AND 3,

AS WELL AS A CONSTRUCT OF SEQ

SEQ ID NOS: 2, 1, 3
IN THAT ORDER.

Point of Contact:
Beverly Shears
Technical Info. Specialist
CM1 12C Tel: 308-4994

THANKS,

[Signature]
CM1 9E03

STAFF USE ONLY

Date completed: 06-16-99
Searcher: Beverly C 4999
Terminal time: 22
Elapsed time: _____
CPU time: _____
Total time: 32
Number of Searches: _____
Number of Databases: 2

Search Site
____ STIC
____ CM-1
____ Pre-S
Type of Search
____ N.A. Sequence
____ A.A. Sequence
____ Structure
____ Bibliographic

Vendors
____ IG
____ STN
____ Dialog
____ APS
____ Geninfo
____ SDC
____ DARC/Questel
____ Other MP

MISCELLANEOUS
***** (TM)

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MParch_pp protein - protein database search, using Smith-Waterman algorithm
Run on: Wed Jun 16 13:13:53 1999; MasPar time 3.60 Seconds
Tabular output not generated. 100.489 Million cell updates/sec

Title: >US-09-027-777B-1
Description: (1-17) from US0902777B.pap
Perfect Score: 137
Sequence: 1 CFGGRMDRIGAQSGLGC 17

Scoring table: PAM 150
Gap 15

Searched: 170751 seqs, 21266608 residues

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database: a-geneseq35
1:part1 2:part2 3:part3 4:part4 5:part5 6:part6 7:part7
8:part8 9:part9 10:part10 11:part11 12:part12 13:part13
14:part14 15:part15 16:part16 17:part17 18:part18
19:part19 20:part20 21:part21 22:part22 23:part23
24:part24 25:part25 26:part26 27:part27 28:part28
29:part29 30:part30 31:part31 32:part32 33:part33
34:part34 35:part35 36:part36 37:part37 38:part38
39:part39

Statistics: Mean 19.929; Variance 62.491; scale 0.319

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description	Pred. No.
1	137	100.0	19	1 P80902	Human cardiolipin f	5.63e-08
2	137	100.0	20	2 R40485	Sequence encoded by h	5.63e-08
3	137	100.0	20	7 R40480	[D-Cys146]hANVP(127-1	5.63e-08
4	137	100.0	21	7 R40641	[Arg129][D-Cys146]hAN	5.63e-08
5	137	100.0	21	7 R40647	[Arg129][D-Ser148]hAN	5.63e-08
6	137	100.0	22	35 W70089	Alpha human atrial na	5.63e-08
7	137	100.0	22	1 P82832	Human Atrial Natriure	5.63e-08
8	137	100.0	22	7 R40846	[Arg129][D-Ser148]hAN	5.63e-08
9	137	100.0	23	7 R40651	[D-Arg129]hANVP(130-1	5.63e-08
10	137	100.0	23	7 R40645	[Arg129][D-Ser148]hAN	5.63e-08
11	137	100.0	23	7 R40395	hANVP(127-149)-NH2	5.63e-08
12	137	100.0	25	2 P71467	Sequence of aldostero	5.63e-08
13	137	100.0	25	7 R40509	[D-Ser128]hANVP(125-1	5.63e-08
14	137	100.0	25	7 R40482	[D-Asn147]hANVP(127-1	5.63e-08
15	137	100.0	25	7 R40475	[D-Cys146]hANVP(127-1	5.63e-08
16	137	100.0	25	7 R40494	[D-Phe149]hANVP(127-1	5.63e-08

17	137	100.0	25	7 R40441	[D-Ala139]hANVP(126-1	5.63e-08
18	137	100.0	25	7 R40489	[D-Asn148]hANVP(127-1	5.63e-08
19	137	100.0	25	7 R40746	[D-Asp136]hANVP(127-1	5.63e-08
20	137	100.0	26	3 P50113	Biologically active s	5.63e-08
21	137	100.0	28	23 W11624	Target peptide from a	5.63e-08
22	137	100.0	28	35 W70087	Alpha human atrial na	5.63e-08
23	137	100.0	28	33 W62656	Human atrial natriure	5.63e-08
24	137	100.0	28	1 R05859	Atrial natriuretic pe	5.63e-08
25	137	100.0	28	3 P50048	Cardionatriin peptide	5.63e-08
26	137	100.0	28	3 P50172	Sequence of alpha-hum	5.63e-08
27	137	100.0	28	10 R37109	Protected linear hANF	5.63e-08
28	137	100.0	28	9 R40042	Leu-(Gly)5-alpha-hANP	5.63e-08
29	137	100.0	28	1 R03415	N-terminal of alpha-h	5.63e-08
30	137	100.0	28	16 R87093	Atrial natriuretic pe	5.63e-08
31	137	100.0	29	22 W13079	Tetradecanoylated atr	5.63e-08
32	137	100.0	29	36 W67041	Atrial natriuretic pe	5.63e-08
33	137	100.0	29	22 W13080	Tetradecanoylated atr	5.63e-08
34	137	100.0	32	36 W67039	Atrial natriuretic pe	5.63e-08
35	137	100.0	32	2 P71466	Sequence of aldostero	5.63e-08
36	137	100.0	35	3 P50112	Biologically active s	5.63e-08
37	137	100.0	35	2 R08328	Chelated atrial natri	5.63e-08
38	137	100.0	40	25 W21945	Fusion protein compri	5.63e-08
39	137	100.0	43	1 P81211	Alpha-human atrial na	5.63e-08
40	137	100.0	126	2 R00582	Human gamma atrial na	5.63e-08
41	137	100.0	126	27 W34533	Human atrial natriure	5.63e-08
42	137	100.0	131	3 R13325	CTA protective peptid	5.63e-08
43	137	100.0	144	4 R21677	Beta-gal leader and p	5.63e-08
44	137	100.0	144	4 R21676	Beta-gal leader and p	5.63e-08
45	137	100.0	151	3 P50050	Cardiodilatin peptide	5.63e-08

ALIGNMENTS

RESULT 1
ID P80902 standard; protein; 19 AA.

AC P80902:
DT 16-OCT-1990 (first entry)
DE Human cardiolipin fragment designated urodilatin (ANF/CDD 95-126)
KW Cardiolipin fragment; urodilatin (ANF/CDD 95-126);
KW ANF/CDD 1-126 (gamma-hANAP); vasodilation; hypertonia; artificial heart;
KW diuretic; renal failure.
OS Homo sapiens.
FH Key Location/Qualifiers
FT disulfide_bond 2..18
FT misc_difference 1
FT /label=OTHER
FT /note=Further peptide fragment of ANF/CDD 1-126
FT /label=OTHER
FT /note=Further peptide fragment of ANF/CDD 1-126
FT misc_difference 19
FT /label=OTHER
FT /note=As above*
PN W08806596-A.
PD 07-SEP-1988.
PF 27-FEB-1988; E00144.
PR 09-DEC-1987; DE-741641,
PR (BISS-) Bissendorf Peptid (FORS/).
PI Forssmann WG, Becker G, Herbst F;
WPI: 88-271140/38.
DR New cardiolipin fragment, urodilatin (ANF/CDD 95-126) -
PT having vasodilating, diuretic and natriuretic activity
PS Claim 1; Page 24; 42pp; German.
CC It has the AA sequence 95-126 of ANF/CDD 1-126 (gamma-hANAP). It may be
CC isolated from human urine by adsorption with alginic acid. It may also be
CC synthesised or prep. by fragment synthesis, e.g. using ANF/CDD 99-126
CC and the tetrapeptide Thr-Ala-Pro-Arg. It can be used in differentiated
CC vasodilation diagnostics and therapy of hypertonia, application as a
CC substn. for patients which have been implanted with artificial hearts &
CC synchronous regulation of blood volume and electrolytes of the blood. It
CC may also be used as a diuretic. It is also suitable for the prophylaxis
CC of an acute renal failure. It is also useful as a diagnostic for
CC differential diagnostics of endothelial changes.
SQ Sequence. 19 AA;

Query Match 100.0%; Score 137; DB 1; Length 19;
 Best Local Similarity 100.0%; Pred. No. 5,63e-08;
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 2 cfiggrmdrigagsglqc 18
 QY 1 CFGGRMDRIGAGSGGLGC 17

RESULT 2
 ID R4085 standard; protein: 20 AA.
 AC R4085;
 DT 01-JUN-1990 (first entry)
 DE Sequence encoded by human natriuretic peptide cDNA.
 KW Porcine BNP; natriuretic; diuretic; vasodilator; hypertension.
 OS Sus scrofa.
 PN W08912069-A.
 PD 14-DEC-1989.
 PF 31-MAY-1989; 02373.
 PR 31-MAY-1988; US-200383.
 PR 14-JUN-1988; US-2006470.
 PR 19-JAN-1989; US-299880.
 PA (CALB) Calif Biotech Inc.
 PI Seilhamer JJ, Lewicki J, Scarborough RM, Porter GJ;
 DR WPI: 90-007453/01.
 DR N-PSDB: Q02846.
 PT New natriuretic and vasodilator peptides - obtd. using cDNA sequence
 PT encoding porcine brain natriuretic peptide and related human and canine
 PT genes.
 PS Example 1; Fig.1: 6lpp; English.
 CC Probes were derived by assuming conservation between human atrial
 CC and porcine brain natriuretic peptide, and used to isolate the pBNP gene.
 CC See also Q02845.
 SQ Sequence 20 AA;

Query Match 100.0%; Score 137; DB 2; Length 20;
 Best Local Similarity 100.0%; Pred. No. 5,63e-08;
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 3 cfiggrmdrigagsglqc 19
 QY 1 CFGGRMDRIGAGSGGLGC 17

RESULT 3
 ID R4080 standard; protein: 20 AA.
 AC R4080;
 DT 14-SEP-1993 (first entry)
 DE [D-Cys146]hANVP(127-146)-NH2
 KW Human; pre-pro: atrial natriuretic/vasodilator peptide; ANVP; rat;
 KW regulation; fluid volume; blood pressure.
 OS Synthetic.
 FH Key Location/Qualifiers
 FT disulfide_bond 4..20
 FT misc_difference 20 /note= "D-form residue"
 FT modified_site 20 /note= "Amidated C-terminal"

US5212286-A.
 ID R4080 standard; protein: 20 AA.
 AC R4080;
 DT 14-SEP-1993 (first entry)
 DE [D-Cys146]hANVP(127-146)-NH2
 KW Human; pre-pro: atrial natriuretic/vasodilator peptide; ANVP; rat;
 KW regulation; fluid volume; blood pressure.
 OS Synthetic.
 FH Key Location/Qualifiers
 FT disulfide_bond 4..20
 FT misc_difference 20 /note= "D-form residue"
 FT modified_site 20 /note= "Amidated C-terminal"

US5212286-A.
 ID R4080 standard; protein: 20 AA.
 AC R4080;
 DT 14-SEP-1993 (first entry)
 DE [D-Cys146]hANVP(127-146)-NH2
 KW Human; pre-pro: atrial natriuretic/vasodilator peptide; ANVP; rat;
 KW regulation; fluid volume; blood pressure.
 OS Synthetic.
 FH Key Location/Qualifiers
 FT disulfide_bond 4..20
 FT misc_difference 20 /note= "D-form residue"
 FT modified_site 20 /note= "Amidated C-terminal"

CC for regulation of fluid volume and blood pressure in host organisms.
 CC These ANVP fragments may be produced by solid-phase techniques. See
 CC also R36937-78.
 SQ Sequence 20 AA;

Query Match 100.0%; Score 137; DB 7; Length 20;
 Best Local Similarity 100.0%; Pred. No. 5,63e-08;
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 4 cfiggrmdrigagsglqc 20
 QY 1 CFGGRMDRIGAGSGGLGC 17

RESULT 4
 ID R40641 standard; protein: 21 AA.
 AC R40641;
 DT 14-SEP-1993 (first entry)
 DE [Arg129][D-Cys146]hANVP(129-149)-NH2
 KW Human; pre-pro: atrial natriuretic/vasodilator peptide; ANVP; rat;
 KW regulation; fluid volume; blood pressure.
 OS Synthetic.
 FH Key Location/Qualifiers
 FT disulfide_bond 2..18
 FT misc_difference 18 /note= "D form residue"
 FT modified_site 21 /note= "Amidated C terminal"

US5212286-A.
 ID R40641 standard; protein: 21 AA.
 AC R40641;
 DT 14-SEP-1993 (first entry)
 DE [Arg129][D-Cys146]hANVP(129-149)-NH2
 KW Human; pre-pro: atrial natriuretic/vasodilator peptide; ANVP; rat;
 KW regulation; fluid volume; blood pressure.
 OS Synthetic.
 FH Key Location/Qualifiers
 FT disulfide_bond 2..18
 FT misc_difference 18 /note= "D form residue"
 FT modified_site 21 /note= "Amidated C terminal"

US5212286-A.
 ID R40641 standard; protein: 21 AA.
 AC R40641;
 DT 14-SEP-1993 (first entry)
 DE [Arg129][D-Cys146]hANVP(129-149)-NH2
 KW Human; pre-pro: atrial natriuretic/vasodilator peptide; ANVP; rat;
 KW regulation; fluid volume; blood pressure.
 OS Synthetic.
 FH Key Location/Qualifiers
 FT disulfide_bond 2..18
 FT misc_difference 18 /note= "D form residue"
 FT modified_site 21 /note= "Amidated C terminal"

Query Match 100.0%; Score 137; DB 7; Length 21;
 Best Local Similarity 100.0%; Pred. No. 5,63e-08;
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 2 cfiggrmdrigagsglqc 18
 QY 1 CFGGRMDRIGAGSGGLGC 17

RESULT 5
 ID R40647 standard; protein: 21 AA.
 AC R40647;
 DT 14-SEP-1993 (first entry)
 DE [Arg129][D-Ser148]hANVP(130-149)-NH2
 KW Human; pre-pro: atrial natriuretic/vasodilator peptide; ANVP; rat;
 KW regulation; fluid volume; blood pressure.
 OS Synthetic.
 FH Key Location/Qualifiers
 FT disulfide_bond 2..18
 FT misc_difference 20 /note= "D-form residue"
 FT modified_site 21 /note= "Amidated C terminal"

US5212286-A.
 ID R40647 standard; protein: 21 AA.
 AC R40647;
 DT 14-SEP-1993 (first entry)
 DE [Arg129][D-Ser148]hANVP(130-149)-NH2
 KW Human; pre-pro: atrial natriuretic/vasodilator peptide; ANVP; rat;
 KW regulation; fluid volume; blood pressure.
 OS Synthetic.
 FH Key Location/Qualifiers
 FT disulfide_bond 2..18
 FT misc_difference 20 /note= "D-form residue"
 FT modified_site 21 /note= "Amidated C terminal"

US5212286-A.
 ID R40647 standard; protein: 21 AA.
 AC R40647;
 DT 14-SEP-1993 (first entry)
 DE [Arg129][D-Ser148]hANVP(130-149)-NH2
 KW Human; pre-pro: atrial natriuretic/vasodilator peptide; ANVP; rat;
 KW regulation; fluid volume; blood pressure.
 OS Synthetic.
 FH Key Location/Qualifiers
 FT disulfide_bond 2..18
 FT misc_difference 20 /note= "D-form residue"
 FT modified_site 21 /note= "Amidated C terminal"

PF 09-APR-1984; 602117.
 PR 09-APR-1984; US-602117.
 PR 01-JUN-1984; US-616488.
 PR 08-MAY-1985; US-766030.
 PR 05-JUN-1986; US-870795.
 PA (SCIO-) SCIOS NOVA INC.
 PI Lewicki JA, Scarborough RM;
 DR WPI; 93-175525/21.
 PT New polypeptide cpd. - useful as natriuretic, diuretic and/or
 PT vasodilator in mammals
 PS Disclosure: Column 49; 45pp; English.
 CC The sequences given in R40367-748 are atrial natriuretic/
 CC vasodilator peptide (ANVP) cDNAs. These ANVP fragments may be used
 CC for regulation of fluid volume and blood pressure in host organisms.
 CC These ANVP fragments may be produced by solid-phase techniques. See
 CC also R36937-78.
 SQ Sequence 21 AA;
 Query Match 100.0%; Score 137; DB 7; Length 21;
 Best Local Similarity 100.0%; Pred. No. 5.63e-08;
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Db 2 cfgrmdrigaqsclgc 18
 |||||
 QY 1 CFGRMDRIGAQSGGLGC 17
 RESULT 6
 ID W70089 standard; peptide; 22 AA.
 AC W70089;
 DE 28-OCT-1998 (first entry)
 DE Alpha human atrial natriuretic peptide (alpha-hANP) 2 (residues 7-28).
 KW ANP; atrial natriuretic peptide; cardiac disease; cardiac hypertrophy;
 KW chronic heart failure; ischaemic cardiac disease; arrhythmia;
 KW cGMP; pulmonary blood circulation; haemodynamic property.
 OS Homo sapiens.
 PN WO9834636-A1.
 PD 13-AUG-1998.
 PF 05-FEB-1998; J00483.
 PR 05-FEB-1997; JP-022594.
 PA (SUNR) SUNTORY LTD.
 PI Furuya M, Hidaka T, Inomata N, Yamaki A;
 DR WPI; 98-446949/38.
 PT Drug composition comprises natriuretic peptide(s) - for safe
 PT treatment of cardiac hypertrophy associated diseases and chronic
 PT heart failure
 PS Examples; Page 23; 35pp; Japanese.
 CC This represents a human alpha atrial natriuretic peptide sequence
 CC (alpha-hANP). The invention provides a composition for treating cardiac
 CC diseases associated with cardiac hypertrophy. The composition comprises
 CC an active ingredient capable of binding to the peptide receptor of GC-A
 CC and promoting production of cGMP. The drug composition may be used
 CC clinically to treat cardiac diseases caused by cardiac hypertrophy,
 CC including chronic heart failure, ischaemic cardiac diseases and
 CC arrhythmia. The active substance can bind to the natriuretic peptide
 CC receptor of GC-A and promote production of cGMP, effectively preventing
 CC cardiac hypertrophy and leading to improvement of the pulmonary blood
 CC circulation. The substance does not affect haemodynamic properties,
 CC blood pressure, heart beat and urine volume.
 SQ Sequence 22 AA;
 Query Match 100.0%; Score 137; DB 35; Length 22;
 Best Local Similarity 100.0%; Pred. No. 5.63e-08;
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Db 1 cfgrmdrigaqsclgc 17
 |||||
 QY 1 CFGRMDRIGAQSGGLGC 17

RESULT 7
 ID P82832 standard; protein; 22 AA.
 AC P82832;
 DT 04-DEC-1990 (first entry)

DE Human Atrial Natriuretic Polypeptide analogue.
 KW Human atrial natriuretic polypeptide; hypotensive; diuretic; beta-LANP.
 OS Synthetic.
 PN EP-266006-A.
 PD 04-MAY-1988.
 PF 26-OCT-1987; 202052.
 PR 27-OCT-1986; JP-255312.
 PA (SHIO) Shionogi Selyaku KK.
 PI Kambayashi Y, Inouye K;
 DR WPI; 88-121118/18.
 PT Human Atrial Natriuretic Polypeptide analogue - having strong diuretic,
 PT natriuretic and hypotensive action.
 PS Claim 1; page 2; 20pp; English.
 CC This sequence differs from that of natural human atrial natriuretic
 CC polypeptide (hANP) in that the N-terminal 6 residues are deleted.
 CC It is present in dimeric form and is useful as a diuretic, natri-
 CC uretic or hypotensive. It has an application in the treatment
 CC or prevention of e.g. cardiac oedema or malignant hypertension.
 CC It is an intermediate for the synthesis of beta-LANP or analogues.
 SQ Sequence 22 AA;
 Query Match 100.0%; Score 137; DB 1; Length 22;
 Best Local Similarity 100.0%; Pred. No. 5.63e-08;
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Db 1 cfgrmdrigaqsclgc 17
 |||||
 QY 1 CFGRMDRIGAQSGGLGC 17

RESULT 8
 ID R40646 standard; Protein; 22 AA.
 AC R40646;
 DT 14-SEP-1993 (first entry)
 DE [Arg129][D-Ser148]hANVP(130-150)-NH2.
 KW Human; pre-pro; atrial natriuretic/vasodilator peptide; ANVP; rat;
 KW regulation; fluid volume; blood pressure.
 OS Synthetic.
 FH Key Location/Qualifiers
 FT disulfide_bond 2..18
 FT misc_difference 20
 FT modified_site 22 /note= "D form residue"
 FT /note= "Amidated C terminal"
 PN US5212286-A.
 PD 18-MAY-1993.
 PF 09-APR-1984; 602117.
 PR 09-APR-1984; US-602117.
 PR 01-JUN-1984; US-616488.
 PR 08-MAY-1985; US-766030.
 PR 05-JUN-1986; US-870795.
 PA (SCIO-) SCIOS NOVA INC.
 PI Lewicki JA, Scarborough RM;
 DR WPI; 93-175525/21.
 PT New polypeptide cpd. - useful as natriuretic, diuretic and/or
 PT vasodilator in mammals
 PS Disclosure: Column 49; 45pp; English.
 CC The sequences given in R40367-748 are atrial natriuretic/
 CC vasodilator peptide (ANVP) cDNAs. These ANVP fragments may be used
 CC for regulation of fluid volume and blood pressure in host organisms.
 CC These ANVP fragments may be produced by solid-phase techniques. See
 CC also R36937-78.
 SQ Sequence 22 AA;
 Query Match 100.0%; Score 137; DB 7; Length 22;
 Best Local Similarity 100.0%; Pred. No. 5.63e-08;
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Db 2 cfgrmdrigaqsclgc 18
 |||||
 QY 1 CFGRMDRIGAQSGGLGC 17

RESULT 9

ID R40651 standard; Protein; 23 AA.
 AC R40651;
 DT 14-SEP-1993 (first entry)
 DE [D-Arg123]hANVP(130-151).
 KW Human; pre-pro; atrial natriuretic/vasodilator peptide; ANVP; rat;
 KW regulation; fluid volume; blood pressure.
 OS Synthetic.
 FH Key Location/Qualifiers
 FT disulfide_bond 2..18
 FT misc_difference 1 /note= "D-form residue"
 FT US5212286-A.
 PN 18-MAY-1993.
 PD 09-APR-1984; 602117.
 PR 09-APR-1984; US-602117.
 PR 01-JUN-1984; US-616488.
 PR 08-MAY-1985; US-766030.
 PR 05-JUN-1986; US-870795.
 PA (SCIO-) SCIOS NOVA INC.
 PI Lewicki JA, Scarborough RM;
 DR WPI; 93-175525/21.
 PT New polypeptide cpd. - useful as natriuretic, diuretic and/or
 PT vasodilator in mammals
 PS Disclosure; Column 49; 45pp; English.
 CC The sequences given in R40387-748 are atrial natriuretic/
 CC vasodilator peptide (ANVP) cDNAs. These ANVP fragments may be used
 CC for regulation of fluid volume and blood pressure in host organisms.
 CC These ANVP fragments may be produced by solid-phase techniques. See
 CC also R36937-78.
 SQ Sequence 23 AA;

Query Match 100.0%; Score 137; DB 7; Length 23;
 Best Local Similarity 100.0%; Pred. No. 5,63e-08;
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 2 cfgrmdrigragsqlgc 18
 |||||
 QY 1 CFGRMDRIGAGSLGC 17

RESULT 10

ID R40645 standard; Protein; 23 AA.
 AC R40645;
 DT 14-SEP-1993 (first entry)
 DE [Arg129][D-Ser148]hANVP(130-151).
 KW Human; pre-pro; atrial natriuretic/vasodilator peptide; ANVP; rat;
 KW regulation; fluid volume; blood pressure.
 OS Synthetic.
 FH Key Location/Qualifiers
 FT disulfide_bond 2..18
 FT misc_difference 20 /note= "D form residue"
 FT US5212286-A.
 PN 18-MAY-1993.
 PD 09-APR-1984; 602117.
 PR 09-APR-1984; US-602117.
 PR 01-JUN-1984; US-616488.
 PR 08-MAY-1985; US-766030.
 PR 05-JUN-1986; US-870795.
 PA (SCIO-) SCIOS NOVA INC.
 PI Lewicki JA, Scarborough RM;
 DR WPI; 93-175525/21.
 PT New polypeptide cpd. - useful as natriuretic, diuretic and/or
 PT vasodilator in mammals
 PS Disclosure; Column 49; 45pp; English.
 CC The sequences given in R40387-748 are atrial natriuretic/
 CC vasodilator peptide (ANVP) cDNAs. These ANVP fragments may be used
 CC for regulation of fluid volume and blood pressure in host organisms.
 CC These ANVP fragments may be produced by solid-phase techniques. See
 CC also R36937-78.
 SQ Sequence 23 AA;

Query Match 100.0%; Score 137; DB 7; Length 23;
 Best Local Similarity 100.0%; Pred. No. 5,63e-08;
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 2 cfgrmdrigragsqlgc 18
 |||||
 QY 1 CFGRMDRIGAGSLGC 17

RESULT 11
 ID R40395 standard; Protein; 23 AA.
 AC R40395;
 DT 14-SEP-1993 (first entry)
 DE hANVP(127-149)-NH2.
 KW Human; pre-pro; atrial natriuretic/vasodilator peptide; ANVP; rat;
 KW regulation; fluid volume; blood pressure.
 OS Synthetic.
 FH Key Location/Qualifiers
 FT disulfide_bond 4..20
 FT modified_site 23 /note= "Amidated C-terminal"
 FT US5212286-A.
 PN 18-MAY-1993.
 PD 09-APR-1984; 602117.
 PR 09-APR-1984; US-602117.
 PR 01-JUN-1984; US-616488.
 PR 08-MAY-1985; US-766030.
 PR 05-JUN-1986; US-870795.
 PA (SCIO-) SCIOS NOVA INC.
 PI Lewicki JA, Scarborough RM;
 DR WPI; 93-175525/21.
 PT New polypeptide cpd. - useful as natriuretic, diuretic and/or
 PT vasodilator in mammals
 PS Disclosure; Column 29; 45pp; English.
 CC The sequences given in R40387-748 are atrial natriuretic/
 CC vasodilator peptide (ANVP) cDNAs. These ANVP fragments may be used
 CC for regulation of fluid volume and blood pressure in host organisms.
 CC These ANVP fragments may be produced by solid-phase techniques. See
 CC also R36937-78.
 SQ Sequence 23 AA;

Query Match 100.0%; Score 137; DB 7; Length 23;
 Best Local Similarity 100.0%; Pred. No. 5,63e-08;
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 4 cfgrmdrigragsqlgc 20
 |||||
 QY 1 CFGRMDRIGAGSLGC 17

RESULT 12
 ID P71467 standard; peptide; 25 AA.
 AC P71467;
 DT 25-APR-1991 (first entry)
 DE Sequence of aldosterone inhibiting polypeptide,
 DE [desArg32]-hANF(8-33).
 KW Aldosterone dependent hypertension; atrial peptide; natriuretic;
 KW diuretic; smooth muscle relaxant.
 OS -
 FH Key Location/Qualifiers
 FT disulfide_bond 5..21
 FT misc_difference 1 /label= H-Arg
 FT misc_difference 25 /label= Tyr-OH
 FT US4643989-A.
 PN 17-FEB-1987.
 PD 17-AUG-1984; 642131.
 PR 17-AUG-1984; US-642131.
 PA (SALK) SALK INST FOR BIOL STUD.
 PI Baird JA.
 DR WPI; 87-064498/09.
 PT Aldosterone inhibiting polypeptide - for controlling aldosterone

PT dependent hypertension
 PS Example; column 11; 14pp; English.
 CC Aldosterone secretion is inhibited by the administration of a
 CC peptide of the invention and its addition salt. It is used for
 CC treatment of aldosterone dependent hypertension. Atrial peptides
 CC have natriuretic, diuretic and smooth muscle relaxant activities.
 SQ Sequence 25 AA;

Query Match 100.0%; Score 137; DB 2; Length 25;
 Best Local Similarity 100.0%; Pred. No. 5.63e-08;
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 5 cfgrmdrigaqsqglgc 21
 |||||
 Qy 1 CFGRMDRIGAQSGLGC 17

RESULT 13
 ID R40509 standard; Protein; 25 AA.
 AC R40509;
 DT 14-SEP-1993 (first entry)
 DE [D-Ser128]rANVP(126-150).
 KW Human; pre-pro; atrial natriuretic/vasodilator peptide; ANVP; rat;
 KW regulation; fluid volume; blood pressure.
 OS Synthetic.
 FH Key Location/Qualifiers
 FT disulfide_bond 4..20
 FT misc_difference 3 /note= "D-form residue"
 FT
 PN US5212286-A.
 PD 18-MAY-1993.
 PF 09-APR-1984; 602117.
 PR 09-APR-1984; US-602117.
 PR 01-JUN-1984; US-616488.
 PR 08-MAY-1985; US-766030.
 PR 05-JUN-1986; US-870795.
 PA (SCIO-) SCIOS NOVA INC.
 PI Lewicki JA, Scarborough RM;
 PI WPI; 93-175525/21.
 DR New polypeptide cpd. - useful as natriuretic, diuretic and/or
 PT vasodilator in mammals
 PS Disclosure; Column 38; 45pp; English.
 CC The sequences given in R40387-748 are atrial natriuretic/
 CC vasodilator peptide (ANVP) cDNAs. These ANVP fragments may be used
 CC for regulation of fluid volume and blood pressure in host organisms.
 CC These ANVP fragments may be produced by solid-phase techniques. See
 CC also R36937-78.
 SQ Sequence 25 AA;

Query Match 100.0%; Score 137; DB 7; Length 25;
 Best Local Similarity 100.0%; Pred. No. 5.63e-08;
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 4 cfgrmdrigaqsqglgc 20
 |||||
 Qy 1 CFGRMDRIGAQSGLGC 17

RESULT 14
 ID R40482 standard; Protein; 25 AA.
 AC R40482;
 DT 14-SEP-1993 (first entry)
 DE [D-Asn147]rANVP(127-151).
 KW Human; pre-pro; atrial natriuretic/vasodilator peptide; ANVP; rat;
 KW regulation; fluid volume; blood pressure.
 OS Synthetic.
 FH Key Location/Qualifiers
 FT disulfide_bond 4..20
 FT misc_difference 21 /note= "D-form residue"
 FT
 PN US5212286-A.
 PD 18-MAY-1993.
 PF 09-APR-1984; 602117.

PR 09-APR-1984; US-602117.
 PR 01-JUN-1984; US-616488.
 PR 08-MAY-1985; US-766030.
 PR 05-JUN-1986; US-870795.
 PA (SCIO-) SCIOS NOVA INC.
 PI Lewicki JA, Scarborough RM;
 PI WPI; 93-175525/21.
 DR New polypeptide cpd. - useful as natriuretic, diuretic and/or
 PT vasodilator in mammals
 PS Disclosure; Column 36; 45pp; English.
 CC The sequences given in R40387-748 are atrial natriuretic/
 CC vasodilator peptide (ANVP) cDNAs. These ANVP fragments may be used
 CC for regulation of fluid volume and blood pressure in host organisms.
 CC These ANVP fragments may be produced by solid-phase techniques. See
 CC also R36937-78.
 SQ Sequence 25 AA;

Query Match 100.0%; Score 137; DB 7; Length 25;
 Best Local Similarity 100.0%; Pred. No. 5.63e-08;
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 4 cfgrmdrigaqsqglgc 20
 |||||
 Qy 1 CFGRMDRIGAQSGLGC 17

RESULT 15
 ID R40475 standard; Protein; 25 AA.
 AC R40475;
 DT 14-SEP-1993 (first entry)
 DE [D-Cys146]hANVP(127-151).
 KW Human; pre-pro; atrial natriuretic/vasodilator peptide; ANVP; rat;
 KW regulation; fluid volume; blood pressure.
 OS Synthetic.
 FH Key Location/Qualifiers
 FT disulfide_bond 4..20
 FT misc_difference 20 /note= "D-form residue"
 FT
 PN US5212286-A.
 PD 18-MAY-1993.
 PF 09-APR-1984; 602117.
 PR 09-APR-1984; US-602117.
 PR 01-JUN-1984; US-616488.
 PR 08-MAY-1985; US-766030.
 PR 05-JUN-1986; US-870795.
 PA (SCIO-) SCIOS NOVA INC.
 PI Lewicki JA, Scarborough RM;
 PI WPI; 93-175525/21.
 DR New polypeptide cpd. - useful as natriuretic, diuretic and/or
 PT vasodilator in mammals
 PS Disclosure; Column 35; 45pp; English.
 CC The sequences given in R40387-748 are atrial natriuretic/
 CC vasodilator peptide (ANVP) cDNAs. These ANVP fragments may be used
 CC for regulation of fluid volume and blood pressure in host organisms.
 CC These ANVP fragments may be produced by solid-phase techniques. See
 CC also R36937-78.
 SQ Sequence 25 AA;

Query Match 100.0%; Score 137; DB 7; Length 25;
 Best Local Similarity 100.0%; Pred. No. 5.63e-08;
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 4 cfgrmdrigaqsqglgc 20
 |||||
 Qy 1 CFGRMDRIGAQSGLGC 17

Search completed: Wed Jun 16 13:14:17 1999
 Job time : 24 secs.

CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 17 amino acids
CC TYPE: amino acid
CC STRANDEDNESS:
CC TOPOLOGY: linear
CC MOLECULE TYPE: peptide
CC SEQUENCE 17 AA: 1728 MW: 1172 CN;

Query Match 100.0%; Score 137; DB 2; Length 17;
Best Local Similarity 100.0%; Pred. No. 4.72e-09;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 1 CFGGRMDRIGASGLGC 17
| | | | | | | | | | | | | | | | | |
Qy 1 CFGGRMDRIGASGLGC 17

RESULT 2
ID 5212286-30 STANDARD; PRT; 21 AA.
XX AC xxxxxx
XX 01-JAN-1900
XX Patent No. 5212286.

XX Patent No. 5212286
CC APPLICANT: LEWICKI, JOHN A.; SCARBOROUGH, ROBERT M.
CC TITLE OF INVENTION: ATRIAL NATRIURETIC/VASODILATOR
CC PEPTIDE COMPOUNDS
CC NUMBER OF SEQUENCES: 68
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: US/07/870,795
CC FILING DATE: 05-JUN-1986
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: 766,030
CC FILING DATE: 08-MAY-1985
CC APPLICATION NUMBER: 602,117
CC FILING DATE: 09-APR-1984
CC APPLICATION NUMBER: 616,488
CC FILING DATE: 01-JUN-1984
CC SEQ ID NO:30:
CC LENGTH: 20
CC SEQUENCE 21 AA: 2168 MW: 1969 CN;

Query Match 100.0%; Score 137; DB 4; Length 20;
Best Local Similarity 100.0%; Pred. No. 4.72e-09;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 4 CFGGRMDRIGASGLGC 20
| | | | | | | | | | | | | | | | | |
Qy 1 CFGGRMDRIGASGLGC 17

RESULT 3
ID 5212286-40 STANDARD; PRT; 24 AA.
XX AC xxxxxx
XX 01-JAN-1900
XX Patent No. 5212286.

XX Patent No. 5212286
CC APPLICANT: LEWICKI, JOHN A.; SCARBOROUGH, ROBERT M.
CC TITLE OF INVENTION: ATRIAL NATRIURETIC/VASODILATOR
CC PEPTIDE COMPOUNDS
CC NUMBER OF SEQUENCES: 68
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: US/07/870,795
CC FILING DATE: 05-JUN-1986
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: 766,030

CC FILING DATE: 08-MAY-1985
CC APPLICATION NUMBER: 602,117
CC FILING DATE: 09-APR-1984
CC APPLICATION NUMBER: 616,488
CC FILING DATE: 01-JUN-1984
CC SEQ ID NO:40:
CC LENGTH: 22
CC SEQUENCE 24 AA: 2609 MW: 2891 CN;

Query Match 100.0%; Score 137; DB 4; Length 22;
Best Local Similarity 100.0%; Pred. No. 4.72e-09;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 2 CFGGRMDRIGASGLGC 18
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Qy 1 CFGGRMDRIGASGLGC 17

RESULT 4
ID 5212286-50 STANDARD; PRT; 25 AA.
XX AC xxxxxx
XX 01-JAN-1900
XX Patent No. 5212286.

XX Patent No. 5212286
CC APPLICANT: LEWICKI, JOHN A.; SCARBOROUGH, ROBERT M.
CC TITLE OF INVENTION: ATRIAL NATRIURETIC/VASODILATOR
CC PEPTIDE COMPOUNDS
CC NUMBER OF SEQUENCES: 68
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: US/07/870,795
CC FILING DATE: 05-JUN-1986
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: 766,030
CC FILING DATE: 08-MAY-1985
CC APPLICATION NUMBER: 602,117
CC FILING DATE: 09-APR-1984
CC APPLICATION NUMBER: 616,488
CC FILING DATE: 01-JUN-1984
CC SEQ ID NO:50:
CC LENGTH: 23
CC SEQUENCE 25 AA: 2627 MW: 3278 CN;

Query Match 100.0%; Score 137; DB 4; Length 23;
Best Local Similarity 100.0%; Pred. No. 4.72e-09;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 4 CFGGRMDRIGASGLGC 20
| | | | | | | | | | | | | | | | | |
Qy 1 CFGGRMDRIGASGLGC 17

RESULT 5
ID 5212286-39 STANDARD; PRT; 25 AA.
XX AC xxxxxx
XX 01-JAN-1900
XX Patent No. 5212286.

XX Patent No. 5212286
CC APPLICANT: LEWICKI, JOHN A.; SCARBOROUGH, ROBERT M.
CC TITLE OF INVENTION: ATRIAL NATRIURETIC/VASODILATOR
CC PEPTIDE COMPOUNDS
CC NUMBER OF SEQUENCES: 68
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: US/07/870,795
CC FILING DATE: 05-JUN-1986
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: 766,030

Wed Jun 16 14:32:23 1999

US-09-027-777B-1.rai

Page 6

Search completed: Wed Jun 16 13:16:53 1999
Job time : 6 secs.

MORF (TM)

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MPsrch_pp protein - protein database search, using Smith-Waterman algorithm
Run on: Wed Jun 16 13:14:33 1999; MasPar time 3.33 Seconds
Tabular output not generated. 204,467 Million cell updates/sec

Title: >US-09-027-777B-1
Description: (1-17) from US0902777B.pap
Perfect Score: 137
Sequence: 1 CFGGRMDRIGAQSGLGC 17

Scoring table: PAM 150
Gap 15

Searched: 122810 seqs, 40068593 residues

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database: pir60
1:pir1 2:pir2 3:pir3 4:pir4

Statistics: Mean 27.474; Variance 37.508; scale 0.732

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB	ID	Description	Pred. No.
1	137	100.0	149	1	AWDG	atrial natriuretic pe	4.27e-18
2	137	100.0	150	1	S13107	atrial natriuretic pe	4.27e-18
3	137	100.0	151	1	AWHU	natriuretic peptide A	4.27e-18
4	137	100.0	152	1	AWBO	atrial natriuretic pe	4.27e-18
5	137	100.0	153	2	S14873	atrial natriuretic pe	4.27e-18
6	137	100.0	161	4	I55480	hypothetical natriure	4.27e-18
7	131	95.6	128	2	S14872	atrial natriuretic pe	1.49e-16
8	128	93.4	152	1	AWRT	atrial natriuretic fa	8.63e-16
9	128	93.4	152	1	AWMS	atrial natriuretic pe	8.63e-16
10	128	93.4	153	1	AWRB	atrial natriuretic pe	8.63e-16
11	118	86.1	30	2	S01657	atrial natriuretic fa	2.82e-13
12	118	86.1	145	2	JO0947	atrial natriuretic pe	2.82e-13
13	112	81.8	36	2	S15821	ventricular natriuret	8.56e-12
14	110	80.3	27	2	A33431	atrial natriuretic fa	2.64e-11
15	106	77.4	27	2	JC1081	brain natriuretic pep	2.46e-10
16	106	77.4	37	2	S71382	lebetin 2 isoform bet	2.46e-10
17	106	77.4	38	2	S71381	lebetin 2 isoform alp	2.46e-10
18	106	77.4	103	2	A41403	aldosterone secretion	2.46e-10
19	106	77.4	105	2	B36736	brain natriuretic pep	2.46e-10
20	106	77.4	115	2	S15822	natriuretic peptide t	2.46e-10
21	106	77.4	131	2	A33873	brain natriuretic pep	2.46e-10
22	106	77.4	131	2	A31676	brain natriuretic fac	2.46e-10
23	104	75.9	22	2	JT0581	natriuretic peptide t	7.44e-10

24	103	75.2	118	2	B54119	C-type natriuretic pe	1.29e-09
25	103	75.2	134	1	AWHUB	natriuretic peptide B	1.29e-09
26	103	75.2	135	2	A61244	natriuretic peptide t	1.29e-09
27	101	73.7	22	2	A36399	C-type natriuretic pe	3.86e-09
28	101	73.7	126	2	S12988	brain natriuretic pep	3.86e-09
29	101	73.7	126	1	AWHUC	natriuretic peptide C	3.86e-09
30	101	73.7	126	2	A55688	natriuretic peptide C	3.86e-09
31	101	73.7	126	2	A36155	natriuretic peptide C	3.86e-09
32	101	73.7	129	2	A54119	C-type natriuretic pep	3.86e-09
33	100	73.0	22	2	A35418	brain natriuretic pep	6.67e-09
34	100	73.0	140	2	S14320	alpha-atrial natriure	6.67e-09
35	90	65.7	121	2	A30162	brain natriuretic fac	1.40e-06
36	86	62.8	121	2	A49144	type-B natriuretic pe	1.12e-05
37	86	62.8	121	2	I45548	brain natriuretic pep	1.12e-05
38	79	57.7	38	2	A42974	natriuretic peptide,	3.86e-04
39	70	51.1	683	2	C71322	probable translation	2.96e-02
40	65	47.4	699	2	B71723	elongation factor G (2.92e-01
41	65	47.4	701	2	S31150	translation elongatio	2.92e-01
42	65	47.4	701	2	E70827	probable fusa protein	2.92e-01
43	64	46.7	787	2	S35701	translation elongatio	4.58e-01
44	62	45.3	819	2	S43748	translation elongatio	1.10e+00
45	61	44.5	302	2	D65054	hypothetical protein	1.69e+00

ALIGNMENTS

RESULT 1
ENTRY #type complete
TITLE atrial natriuretic peptide precursor - dog
ALTERNATE_NAMES ANP; atrial natriuretic polypeptide
ORGANISM #formal_name Canis lupus familiaris.#common_name dog
DATE 31-Mar-1988 #sequence_revision 31-Mar-1988 #text_change 22-Jan-1999
ACCESSIONS A25302
REFERENCE A90119
#authors Oikawa, S.; Imai, M.; Inuzuka, C.; Tawaragi, Y.; Nakazato, H.; Matsuo, H.
#journal Biochem. Biophys. Res. Commun. (1985) 132:892-899
#title Structure of dog and rabbit precursors of atrial natriuretic polypeptides deduced from nucleotide sequence of cloned cDNA.
#cross-references MUID:86076957
#accession A25302
#molecule_type mRNA
#residues 1-149 #label OIK
#cross-references GB:M12045; NID:g163900; PID:g163901
CLASSIFICATION #superfamily natriuretic peptide A precursor
KEYWORDS atrium; diuretic; hormone; natriuretic; osmoregulation
FEATURE
1-23 #domain signal sequence #status predicted #label SIG\
24-149 #product gamma atrial natriuretic factor #status predicted #label ANP\
122-149 #product alpha atrial natriuretic peptide #status predicted #label ANP\
128-144 #disulfide_bonds #status predicted
SUMMARY #length 149 #molecular_weight 15819 #checksum 8040
Query Match 100.0%; Score 137; DB 1; Length 149;
Best Local Similarity 100.0%; Pred. No. 4.27e-18;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Db 128 CFGGRMDRIGAQSGLGC 144
|||||
QY 1 CFGGRMDRIGAQSGLGC 17
RESULT 2
ENTRY #type complete
TITLE atrial natriuretic peptide precursor - pig
CONTAINS alpha atrial natriuretic peptide; gamma atrial natriuretic factor (cardiolipatin)
ORGANISM #formal_name Sus scrofa domestica.#common_name domestic pig
DATE 21-Nov-1993 #sequence_revision 14-Jul-1994 #text_change

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20-Mar-1998
S13107; A60899
REFERENCE
#authors
#journal
#title
Nucleotide sequence of a porcine prepro atrial natriuretic
peptide (ANP) cDNA.
#cross-references MUID:91067478
#accession S13107
#molecule_type mRNA
#residues 1-150 #label MAE
#cross-references ENBL:X54669; NID:g1883; PID:g1884
A60899
#authors
Forssmann, W.G.; Hock, D.; Lottspeich, A.; Henschen, A.;
Kreye, V.; Christmann, M.; Reinecke, M.; Metz, J.;
Carlquist, M.; Mutt, V.
#journal
Anat. Embryol. (1983) 168:307-313
#title
The right auricle of the heart is an endocrine organ.
Cardiodilatin as a peptide hormone candidate.
#accession A60899
#molecule_type Protein
#residues 25-54 #label FOR
CLASSIFICATION
#superfamily natriuretic peptide A precursor
KEYWORDS
atrium; diuretic; hormone; natriuretic; osmoregulation
FEATURE
1-24 #domain signal sequence #status predicted #label SIG\
25-150 #product gamma atrial natriuretic factor #status
predicted #label ANF\
123-150 #product alpha atrial natriuretic peptide #status
predicted #label ANP\
129-145 #disulfide_bonds #status predicted
#length 150 #molecular_weight 16351 #checksum 9859
SUMMARY
Query Match 100.0%; Score 137; DB 1; Length 150;
Best Local Similarity 100.0%; Pred. No. 4.27e-18;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Db 129 CFGGRMDRIGAGSLGC 145
|||||
Oy 1 CFGGRMDRIGAGSLGC 17

RESULT 3
ENTRY
#type complete
TITLE
natriuretic peptide A precursor - human
ALTERNATE_NAMES
ANF; atrial natriuretic factor; atrial natriuretic protein;
preonatriodilatin (PND)
CONTAINS
atrial alpha natriuretic peptide (ANP); cardiodilatin (atrial
gamma natriuretic factor)
ORGANISM
#formal_name Homo sapiens #common_name man
DATE
15-Nov-1984 #sequence_revision 15-Nov-1984 #text_change
20-Mar-1998
A22693; B22693; A01424; B29370; A32733; I58054; S14097;
I39458; I39459; I39460; I37167
A22693
#authors
Nemer, M.; Chamberland, M.; Sirois, D.; Argentin, S.; Drouin,
J.; Dixon, R.A.F.; Zivin, R.A.; Condra, J.H.
#journal
Nature (1984) 312:654-656
#title
Gene structure of human cardiac hormone precursor,
pronatriodilatin.
#cross-references MUID:85061626
#accession A22693
#molecule_type DNA
#residues 1-151 #label NEM
#cross-references GB:X01470; NID:g28687; PID:g825625
A22693
#accession
#molecule_type DNA
#residues 1-151, 'RR' #label NE2
#note
allelic variant with UGA termination codon replaced by
CGA arginine codon
REFERENCE
A01424
#authors
Oikawa, S.; Imai, M.; Ueno, A.; Tanaka, S.; Noguchi, T.;
Nakazato, H.; Kangawa, K.; Fukuda, A.; Matsuo, H.

```

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#journal
Nature (1984) 309:724-726
#title
Cloning and sequence analysis of cDNA encoding a precursor
for human atrial natriuretic polypeptide.
#cross-references MUID:84219799
#accession A01424
#molecule_type mRNA
#residues 1-151 #label OIK
#cross-references GB:K02043; NID:g178629; PID:g178630
A29370
#authors
Seidman, C.E.; Bloch, K.D.; Klein, K.A.; Smith, J.A.;
Seidman, J.G.
#journal
Science (1984) 226:1206-1209
#title
Nucleotide sequences of the human and mouse atrial
natriuretic factor genes.
#cross-references MUID:85065766
#accession B29370
#molecule_type DNA
#residues 1-64, 'D', 66-151 #label SEI
#cross-references GB:K02043
A32733
#authors
Kangawa, K.; Matsuo, H.
#journal
Biochem. Biophys. Res. Commun. (1984) 118:131-139
#title
Purification and complete amino acid sequence of alpha-human
atrial natriuretic polypeptide (alpha-hANP).
#cross-references MUID:84128019
#accession A32733
#molecule_type Protein
#residues 124-151 #label KAN
I58054
#authors
Nakayama, K.; Ohkubo, H.; Hirose, T.; Inayama, S.; Nakanishi,
S.
#journal
Nature (1984) 310:699-701
#title
mRNA sequence for human cardiodilatin-atrial natriuretic
factor precursor and regulation of precursor mRNA in rat
atria.
#cross-references MUID:84295577
#accession I58054
#status translated from GB/EMBL/DBDJ
#molecule_type mRNA
#residues 1-151 #label RES
#cross-references GB:M30262; NID:g180181; PID:g180182
S14097
#authors
Vanneste, Y.; Michel, A.; Deschodt-Lanckman, M.
#journal
Eur. J. Biochem. (1991) 196:281-286
#title
Hydrolysis of intact and Cys-Phe-cleaved human atrial
natriuretic peptide in vitro by human tissue kallikrein.
#cross-references MUID:51176998
#accession S14097
#molecule_type Protein
#residues 124-151 #label VAN
#note
natural and synthetic peptide subjected to kallikrein
proteolysis
I39458
#authors
Zivin, R.A.; Condra, J.H.; Dixon, R.A.; Seidah, N.G.;
Chretien, M.; Nemer, M.; Chamberland, M.; Drouin, J.
#journal
Proc. Natl. Acad. Sci. U.S.A. (1984) 81:6325-6329
#title
Molecular cloning and characterization of DNA sequences
encoding rat and human atrial natriuretic factors.
#cross-references MUID:85038509
#accession I39458
#status preliminary; translated from GB/EMBL/DBDJ
#molecule_type mRNA
#residues 119-151, 'RR' #label RE2
#cross-references GB:K02044; NID:g178631; PID:g178632
I39459
#authors
Maki, M.; Parmentier, M.; Inagami, T.
#journal
Biochem. Biophys. Res. Commun. (1984) 125:797-802
#title
Cloning of genomic DNA for human atrial natriuretic factor.
#cross-references MUID:85096983
#accession I39459
#status preliminary; translated from GB/EMBL/DBDJ
#molecule_type DNA
#residues 1-75 #label RE3

```

```

##cross-references GB:K02399; NID:gl78633; PID:gl78634
REFERENCE
I39460
#authors
Seidman, C.E.; Bloch, K.D.; Zisfein, J.; Smit, J.; Haber, E.;
Honey, C.J.; Duby, A.D.; Choi, E.; Graham, R.M.; Seidman,
J.G.
#journal
Hypertension (1985) 7:31-34
#accession
I39460
#status
translated from GB/EMBL/DBJ
#molecule_type DNA
#residues 1-64,'D',66-151 #label RE4
##cross-references GB:M54951; NID:gl78636; PID:gl78638
REFERENCE
I37167
#authors
Greenberg, B.D.; Bencen, G.H.; Seilhamer, J.J.; Lewicki,
J.A.; Fiddes, J.C.
#journal
Nature (1984) 312:656-658
#title
Nucleotide sequence of the gene encoding human atrial
natriuretic factor precursor.
##cross-references MUID:85061627
#accession
I37167
#status
translated from GB/EMBL/DBJ
#molecule_type DNA
#residues 26-151 #label RE5
##cross-references EMBL:X01471; NID:g28690
COMMENT Cardiolipin is a vasoconstrictor but not a diuretic or
natriuretic.
GENETICS
#gene
GDB:NPPA; ANP; PND
##cross-references GDB:118727; OMIM:108780
#map_position 1p36-1p36
#introns 41/3; 150/3
CLASSIFICATION
#superfamily natriuretic peptide A precursor
KEYWORDS
atrium; diuretic; hormone; natriuretic; osmoregulation
FEATURE
1-25 #domain signal sequence #status predicted #label SIG\
26-151 #product cardiolipin #status predicted #label SIG\
124-151 #product atrial alpha natriuretic peptide #status
experimental #label ANP\
130-146 #disulfide_bonds #status experimental
SUMMARY
#length 151 #molecular-weight 16395 #checksum 3644
Query Match 100.0%; Score 137; DB 1; Length 151;
Best Local Similarity 100.0%; Pred. No. 4.27e-18;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Db 130 CFGGRMDRIGAQSGLGC 146
QY 1 CFGGRMDRIGAQSGLGC 17
RESULT 4
ENTRY AWBO #type complete
TITLE atrial natriuretic peptide precursor - bovine
ALTERNATE_NAMES ANP; atrial natriuretic polypeptide
ORGANISM #formal_name Bos primigenius taurus #common_name cattle
DATE 30-Jun-1989 #sequence_revision 30-Jun-1989 #text_change
20-Mar-1998
ACCESSIONS A90124; A93049; A24247; A26090
REFERENCE A90124
#authors
Viasuk, G.P.; Miller, J.; Bencen, G.H.; Lewicki, J.A.
#journal
Biochem. Biophys. Res. Commun. (1986) 136:396-403
#title
Structure and analysis of the bovine atrial natriuretic
peptide precursor gene.
##cross-references MUID:85215205
#accession
A90124
#molecule_type DNA
#residues 1-152 #label VLA
##cross-references GB:M13145; NID:g162665; PID:g162666
REFERENCE A93049
#authors
Ong, H.; McNicoll, N.; Lazure, C.; Seidah, N.; Chretien, M.;
Cantin, M.; De Lean, A.
#journal
Life Sci. (1986) 38:1309-1315
#title
Purification and sequence determination of bovine atrial
natriuretic factor.
##cross-references MUID:86173941
#accession A93049
#molecule_type protein
#residues 123-150 #label ONG
GENETICS
#introns 40/3; 149/3
CLASSIFICATION
#superfamily natriuretic peptide A precursor
KEYWORDS
atrium; diuretic; hormone; natriuretic; osmoregulation
FEATURE
1-24 #domain signal sequence #status predicted #label SIG\
25-152 #product gamma atrial natriuretic factor #status
predicted #label ANP\
123-150 #product alpha atrial natriuretic peptide #status
experimental #label ANP\
129-145 #disulfide_bonds #status predicted
SUMMARY
#length 152 #molecular-weight 16518 #checksum 7552
Query Match 100.0%; Score 137; DB 1; Length 152;
Best Local Similarity 100.0%; Pred. No. 4.27e-18;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Db 129 CFGGRMDRIGAQSGLGC 145
QY 1 CFGGRMDRIGAQSGLGC 17
RESULT 5
ENTRY S14873 #type complete
TITLE atrial natriuretic peptide precursor - horse
ORGANISM #formal_name Equus caballus #common_name domestic horse
DATE 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change
08-Sep-1997
ACCESSIONS S14873
REFERENCE S14872
#authors
Maegert, H.J.; Hanke, M.; Schmeding, G.; Teuteberg, K.;
Schulz-Knappe, P.; Forssmann, W.G.
#submission
submitted to the EMBL Data Library, March 1991
#accession
S14873
#status preliminary
#molecule_type mRNA
#residues 1-153 #label MAE
##cross-references EMBL:X58563; NID:gl1008; PID:gl1009
CLASSIFICATION
#superfamily natriuretic peptide A precursor
SUMMARY
#length 153 #molecular-weight 16825 #checksum 960
Query Match 100.0%; Score 137; DB 2; Length 153;
Best Local Similarity 100.0%; Pred. No. 4.27e-18;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Db 130 CFGGRMDRIGAQSGLGC 146
QY 1 CFGGRMDRIGAQSGLGC 17
RESULT 6
ENTRY I55480 #type complete
TITLE hypothetical natriuretic peptide/phage fr coat protein mutant
fusion protein - synthetic
ORGANISM #formal_name synthetic
#note Homo sapiens (man) and phage fr genes engineered and
expressed in Escherichia coli
DATE 02-Jul-1996 #sequence_revision 05-Sep-1996 #text_change
05-Sep-1996
ACCESSIONS I55480
REFERENCE I55480
#authors
Berzins, V.; Jansone, I.; Skangals, A.; Kalnins, P.; Liepa,
S.; Baumanis, V.
#journal
J. Biotechnol. (1993) 30:231-243
#title
High level expression of alpha-human atrial natriuretic
factor as a fusion polypeptide with phage fr coat protein
in Escherichia coli.
#accession
I55480

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##status preliminary; translated from GB/EMBL/DDBJ
##molecule_type DNA
##residues 1-161 ##label RES
##cross-references GB:566567; NID:g435742; PID:g435743
KEYWORDS fusion protein
SUMMARY #length 161 #molecular-weight 17287 #checksum 337

Query Match
Best Local Similarity 100.0%; Score 137; DB 4; Length 161;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 140 CFGGRMDRIGAQSLG 156
QY 1 CFGGRMDRIGAQSLG 17
|||||
|||||

RESULT 7
ENTRY #type fragment
TITLE atrial natriuretic peptide precursor - guinea pig (fragment)
ORGANISM #formal_name Cavia porcellus #common_name guinea pig
DATE 20-Feb-1995 #sequence_revision 30-Jan-1998 #text_change
20-Mar-1998
ACCESSIONS S14872
REFERENCE #authors Maegert, H.J.; Hanke, M.; Schmieding, G.; Teuteberg, K.;
Schulz-Knappe, P.; Forssmann, W.G.
#submission submitted to the EMBL Data Library, March 1991
#accession S14872
##molecule_type mRNA
##residues 1-128 ##label MAE
##cross-references EMBL:X58562; NID:g49543; PID:g49544
##experimental_source heart atria; adult
CLASSIFICATION #superfamily natriuretic peptide A precursor
KEYWORDS atrium; diuretic; hormone; natriuretic; osmoregulation
FEATURE
1-98 #domain signal sequence #status predicted #label SIG\
99-128 #product atrial natriuretic peptide #status predicted
#label MAT\
105-121 #disulfide_bonds #status predicted
SUMMARY #length 128 #checksum 8741

Query Match
Best Local Similarity 95.68; Score 131; DB 2; Length 128;
Matches 16; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Db 105 CFGGRMDRIGAQSLG 121
QY 1 CFGGRMDRIGAQSLG 17
|||||
|||||

RESULT 8
ENTRY #type complete
TITLE atrial natriuretic factor precursor - rat
CONTAINS ANF(1-33); ANF(2-33); ANF(3-33); ANF(8-33); atrial
natriuretic peptide; atriopeptin I; atriopeptin II;
auriculin A; auriculin B; preprocardionatriin
ORGANISM #formal_name Rattus norvegicus #common_name Norway rat
DATE 19-Feb-1984 #sequence_revision 15-Nov-1984 #text_change
26-Feb-1999
ACCESSIONS A22570; A01425; A93332; A43617; A93330; A94275; PT0061;
A20973; A44190; A60390; I59094; I58057; I52678
REFERENCE #authors Argentin, S.; Nemer, M.; Drouin, J.; Scott, G.K.; Kennedy,
B.P.; Davies, P.L.
#journal J. Biol. Chem. (1985) 260:4568-4571
#title The gene for rat atrial natriuretic factor.
#cross-references MUID:85182558
#accession A22570
##molecule_type DNA
##residues 1-152 ##label ARG
##cross-references GB:K02062; NID:g202899; PID:g202900
REFERENCE #authors Yamanaka, M.; Greenberg, B.; Johnson, L.; Seilhamer, J.;

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Brewer, M.; Friedemann, T.; Miller, J.; Atlas, S.; Laragh,
J.; Lewicki, J.; Fiddes, J.
Nature (1984) 309:719-722
Cloning and sequence analysis of the cDNA for the rat atrial
natriuretic factor precursor.
#cross-references MUID:84219797
#accession A01425
##molecule_type mRNA
##residues 1-152 ##label YAM
##cross-references EMBL:X00665; NID:g55711; PID:g55712
REFERENCE A93332
#authors Maki, M.; Takayanagi, R.; Misono, K.S.; Pandey, K.N.;
Tibbets, C.; Inagami, T.
#journal Nature (1984) 309:722-724
#title Structure of rat atrial natriuretic factor precursor deduced
from cDNA sequence.
#cross-references MUID:84219798
#accession A93332
##molecule_type mRNA
##residues 1-152 ##label MAK
##cross-references GB:X00665; EMBL:X00658; NID:g55711; PID:g55712
REFERENCE A43617
#authors Seidman, C.E.; Duby, A.D.; Choi, E.; Graham, R.M.; Haber, E.;
Homcy, C.; Smith, J.A.; Seidman, J.G.
#journal Science (1984) 225:324-326
#title The structure of rat preproatrial natriuretic factor as
defined by a complementary DNA clone.
#cross-references MUID:84250178
#accession A43617
##molecule_type mRNA
##residues 1-152 ##label SEI
##cross-references GB:K02062; GB:K02063; NID:g202899; PID:g202900
REFERENCE A93330
#authors Atlas, S.A.; Kleinert, H.D.; Camargo, M.J.; Januszewicz, A.;
Sealey, J.E.; Laragh, J.H.; Schilling, J.W.; Lewicki, J.A.;
Johnson, L.K.; Maack, T.
#journal Nature (1984) 309:717-719
#title Purification, sequencing and synthesis of natriuretic and
vasoactive rat atrial peptide.
#cross-references MUID:84219796
#accession A93330
##molecule_type protein
##residues 126-149 ##label ATL
REFERENCE A94275
#authors Currie, M.S.; Geller, D.M.; Cole, B.R.; Siegel, N.R.; Fok,
K.F.; Adams, S.P.; Eubanks, S.R.; Galluppi, G.R.;
Needleman, P.
#journal Science (1984) 223:67-69
#title Purification and sequence analysis of bioactive atrial
peptides (atriopeptins).
#cross-references MUID:84097513
#accession A94275
##molecule_type protein
##residues 127-149 ##label CUR
REFERENCE PT0061
#authors Thibault, G.; Murthy, K.K.; Gutkowska, J.; Seidah, N.G.;
Lazure, C.; Chretien, M.; Cantin, M.
#journal Peptides (1988) 9:47-53
#title NH2-terminal fragment of rat pro-atrial natriuretic factor in
the circulation: identification, radioimmunoassay and
half-life.
#cross-references MUID:88203350
#accession PT0061
##molecule_type protein
##residues 25-38, 'X', 33, 'X', 35-38 ##label THI
REFERENCE A20973
#authors Seldah, N.G.; Lazure, C.; Chretien, M.; Thibault, G.; Garcia,
R.; Cantin, M.; Genest, J.; Nutt, R.F.; Brady, S.F.; Lyle,
T.A.; Paleveda, W.J.; Colton, C.D.; Ciccarone, T.M.; Veber,
D.F.
#journal Proc. Natl. Acad. Sci. U.S.A. (1984) 81:2640-2644
#title Amino acid sequence of homologous rat atrial peptides:
natriuretic activity of native and synthetic forms.

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#cross-references MUID:84194062
#accession Az0973
#molecule_type protein
#residues 118-150 #label SE2
REFERENCE
#authors Flynn, T.G.; Davies, P.L.; Kennedy, B.P.; de Boid, M.L.; de
Bold, A.J.
#journal Science (1985) 228:323-325
#title Alignment of rat cardionatrin sequences with the
preprocardionatrin sequence from complementary DNA.
#cross-references MUID:85168263
#accession A44190
#molecule_type mRNA
#residues 1-152 #label FLY
#cross-references GB:K02062; NID:g202899; PID:g202900
#note part of this sequence, including the amino ends of three
mature peptides, was confirmed by protein sequencing
REFERENCE
#authors Belcourt, D.; Varma, D.R.; Toney, K.; Bennett, H.P.J.
#journal Protein Expr. Purif. (1990) 1:28-32
#title Purification of rat pro-atrial natriuretic factor: a
simplified scheme using reversed-phase high-performance
liquid chromatography.
#cross-references MUID:93044510
#accession A60390
#molecule_type protein
#residues 25-39 #label BEL
REFERENCE
#authors Gardner, D.G.; Vlasuk, G.P.; Baxter, J.D.; Fiddes, J.C.;
Lewicki, J.A.
#journal Proc. Natl. Acad. Sci. U.S.A. (1987) 84:2175-2179
#title Identification of atrial natriuretic factor gene transcripts
in the central nervous system of the rat.
#cross-references MUID:8715636
#accession I59094
#status translated from GB/EMBL/DBJ
#molecule_type mRNA
#residues 38-152 #label RES
#cross-references GB:M15868; NID:g202903; PID:g202904
REFERENCE
#authors Kangawa, K.; Tawaragi, Y.; Oikawa, S.; Mizuno, A.;
Sakuragawa, Y.; Nakazato, H.; Fukuda, A.; Minamino, N.;
Matsuo, H.
#journal Nature (1984) 312:152-155
#title Identification of rat gamma atrial natriuretic polypeptide
and characterization of the cDNA encoding its precursor.
#cross-references MUID:85061500
#accession I58057
#status preliminary; translated from GB/EMBL/DBJ
#molecule_type mRNA
#residues 1-152 #label RE2
#cross-references EMBL:X01118; NID:g55716; PID:g55717
REFERENCE
#authors Flynn, T.G.
#journal Can. J. Physiol. Pharmacol. (1987) 65:2013-2020
#title The elucidation of the structure of atrial natriuretic
factor, a new peptide hormone.
#cross-references MUID:88109092
#accession I52678
#status preliminary; translated from GB/EMBL/DBJ
#molecule_type mRNA
#residues 1-51, 'X', 53-85, 'X', 87-152 #label RE3
#cross-references GB:M27498; NID:g202905; PID:g202906
COMMENT A disulfide bond is required for full activity of atriopeptins.
COMMENT Several active peptides may be derived from the carboxyl region of
this precursor.
GENETICS
#gene ANF
#introns 40/3; 149/3
CLASSIFICATION #superfamily natriuretic peptide A precursor
KEYWORDS atrium; diuretic; hormone; natriuretic; osmoregulation
FEATURE
1-24 #domain signal sequence #status predicted #label SIG\
#product gamma atrial natriuretic factor #status
predicted #label ANF\
#product alpha atrial natriuretic peptide #status
predicted #label ANP\
#disulfide_bonds #status predicted
#length 152 #molecular-weight 16645 #checksum 9384
Query Match 93.4%; Score 128; DB 1; Length 152;
Best Local Similarity 94.1%; Pred. NO. 8.63e-16;
Matches 16; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
Db 129 CFGGRMDRIGAQSGLGC 145
|||||:|||||
Oy 1 CFGGRMDRIGAQSGLGC 17

RESULT 9
ENTRY #type complete
TITLE atrial natriuretic peptide precursor - mouse
ORGANISM #formal_name Mus musculus #common_name house mouse
DATE 31-Mar-1988 #sequence_revision 31-Mar-1988 #text_change
20-Mar-1998
ACCESSIONS A29370; B43619
REFERENCE A29370
#authors Seidman, C.E.; Bloch, K.D.; Klein, K.A.; Smith, J.A.;
Seidman, J.G.
#journal Science (1984) 226:1206-1209
#title Nucleotide sequences of the human and mouse atrial
natriuretic factor genes.
#cross-references MUID:85063766
#accession A29370
#molecule_type DNA
#residues 1-152 #label SEI
#cross-references GB:K02781; NID:g191937; PID:g387099
GENETICS
#introns 40/3; 149/3
CLASSIFICATION #superfamily natriuretic peptide A precursor
KEYWORDS atrium; diuretic; hormone; natriuretic; osmoregulation
FEATURE
1-24 #domain signal sequence #status predicted #label SIG\
#product gamma atrial natriuretic factor #status
predicted #label ANF\
#product alpha atrial natriuretic peptide #status
predicted #label ANP\
#disulfide_bonds #status predicted
#length 152 #molecular-weight 16645 #checksum 9384
Query Match 93.4%; Score 128; DB 1; Length 152;
Best Local Similarity 94.1%; Pred. NO. 8.63e-16;
Matches 16; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
Db 129 CFGGRMDRIGAQSGLGC 145
|||||:|||||
Oy 1 CFGGRMDRIGAQSGLGC 17

RESULT 10
ENTRY #type complete
TITLE atrial natriuretic peptide precursor - rabbit
ALTERNATE_NAMES ANP; atrial natriuretic polypeptide

```

```

#product pro-atrial natriuretic factor #status
experimental #label PRO\
#product cardionatrin IV #status experimental #label
CN4\
#product cardionatrin III #status experimental #label
CN3\
#product ANF(1-33) #status experimental #label ANF1\
#product ANF(2-33) #status experimental #label ANF2\
#product ANF(3-33) #status experimental #label ANF3\
#product cardionatrin I #status experimental #label CN1\
#product ANF(8-33) #status experimental #label ANF4\
#product auriculin B #status experimental #label AUB\
#product auriculin A #status experimental #label AUA\
#product atrial natriuretic factor #status predicted
#label MAT\
#product atriopeptin I #status experimental #label AT1\
#product atriopeptin II #status experimental #label AT2\
#disulfide_bonds #status experimental
#length 152 #molecular-weight 16356 #checksum 7818
Query Match 93.4%; Score 128; DB 1; Length 152;
Best Local Similarity 94.1%; Pred. NO. 8.63e-16;
Matches 16; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
Db 129 CFGGRMDRIGAQSGLGC 145
|||||:|||||
Oy 1 CFGGRMDRIGAQSGLGC 17

RESULT 9
ENTRY #type complete
TITLE atrial natriuretic peptide precursor - mouse
ORGANISM #formal_name Mus musculus #common_name house mouse
DATE 31-Mar-1988 #sequence_revision 31-Mar-1988 #text_change
20-Mar-1998
ACCESSIONS A29370; B43619
REFERENCE A29370
#authors Seidman, C.E.; Bloch, K.D.; Klein, K.A.; Smith, J.A.;
Seidman, J.G.
#journal Science (1984) 226:1206-1209
#title Nucleotide sequences of the human and mouse atrial
natriuretic factor genes.
#cross-references MUID:85063766
#accession A29370
#molecule_type DNA
#residues 1-152 #label SEI
#cross-references GB:K02781; NID:g191937; PID:g387099
GENETICS
#introns 40/3; 149/3
CLASSIFICATION #superfamily natriuretic peptide A precursor
KEYWORDS atrium; diuretic; hormone; natriuretic; osmoregulation
FEATURE
1-24 #domain signal sequence #status predicted #label SIG\
#product gamma atrial natriuretic factor #status
predicted #label ANF\
#product alpha atrial natriuretic peptide #status
predicted #label ANP\
#disulfide_bonds #status predicted
#length 152 #molecular-weight 16645 #checksum 9384
Query Match 93.4%; Score 128; DB 1; Length 152;
Best Local Similarity 94.1%; Pred. NO. 8.63e-16;
Matches 16; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
Db 129 CFGGRMDRIGAQSGLGC 145
|||||:|||||
Oy 1 CFGGRMDRIGAQSGLGC 17

RESULT 10
ENTRY #type complete
TITLE atrial natriuretic peptide precursor - rabbit
ALTERNATE_NAMES ANP; atrial natriuretic polypeptide

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ORGANISM      #formal_name Oryctolagus cuniculus #common_name domestic
               rabbit
DATE          31-Mar-1988 #sequence_revision 31-Mar-1988 #text_change
               20-Mar-1998
ACCESSIONS    B25302
REFERENCE      A90119
#authors      Oikawa, S.; Imai, M.; Inuzuka, C.; Tawaragi, Y.; Nakazato,
               H.; Matsuo, H.
#journal      Biochem. Biophys. Res. Commun. (1985) 132:892-899
#title        Structure of dog and rabbit precursors of atrial natriuretic
               polypeptides deduced from nucleotide sequence of cloned
               cDNA.
#cross-references MUID:86076957
#accession    B25302
#molecule_type mRNA
#residues     1-153 #label OIK
#cross-references GB:M12046; NID:g164770; PID:g164771
CLASSIFICATION #superfamily natriuretic peptide A precursor
KEYWORDS       atrium; diuretic; hormone; natriuretic; osmoregulation
FEATURE        1-25      #domain signal sequence #status predicted #label SIG\
26-151          #product gamma atrial natriuretic factor #status
124-151          #product alpha atrial natriuretic peptide #status
130-146          #disulfide_bonds #status predicted
SUMMARY        #length 153 #molecular_weight 16843 #checksum 7650
Query Match    93.4%; Score 128; DB 1; Length 153;
Best Local Similarity 94.1%; Pred. No. 8.63e-16;
Matches 16; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Db 130 CFGGRMDRIGAQSGLCG 146
Qy 1 CFGGRMDRIGAQSGLCG 17

RESULT 11
ENTRY   S01657 #type fragment
TITLE   atrial natriuretic factor - laughing frog (fragment)
ALTERNATE_NAMES
ORGANISM atriopeptin
DATE     01-Dec-1989 #sequence_revision 01-Dec-1989 #text_change
09-Dec-1994
ACCESSIONS S01657; A30977
REFERENCE   S01657
#authors    Lazure, C.; Ong, H.; McNicoll, N.; Netchitallo, P.; Chretien,
               M.; de Lean, A.; Vaudry, H.
#journal    FEBS Lett. (1988) 238:300-306
#title      The amino acid sequences of frog heart atrial
               natriuretic-like peptide and mammalian ANF are closely
               related.
#cross-references MUID:89005705
#accession    S01657
#molecule_type protein
#residues     1-50 #label LAZ
#note         the sequence from the summary is inconsistent with that
               from Fig. 3 in lacking residues 3-6
CLASSIFICATION #superfamily natriuretic peptide A precursor
SUMMARY        #length 30 #checksum 4650

Query Match    86.1%; Score 118; DB 2; Length 30;
Best Local Similarity 82.4%; Pred. No. 2.82e-13;
Matches 14; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Db 11 CFGSRIDRIGAQSGMGC 27
Qy 1 CFGGRMDRIGAQSGLCG 17

RESULT 12
ENTRY   J00947 #type complete
TITLE   atrial natriuretic peptide precursor - bullfrog

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ALTERNATE_NAMES ANP: atrial natriuretic factor (ANF)
CONTAINS         atrial natriuretic peptide-21; atrial natriuretic peptide-24
ORGANISM          #formal_name Rana catesbeiana #common_name bullfrog
DATE             30-Sep-1991 #sequence_revision 30-Sep-1991 #text_change
               20-Mar-1998
ACCESSIONS       J00947; A31510
REFERENCE         J00947
#authors          Kojima, M.
#submission       submitted to JIPID, May 1991
#accession        J00947
#molecule_type  mRNA
#residues         1-145 #label KOJ
REFERENCE         A31510
#authors          Sakata, J.; Kangawa, K.; Matsuo, H.
#journal          Biochem. Biophys. Res. Commun. (1988) 155:1338-1345
#title            Identification of new atrial natriuretic peptides in frog
               heart.
#cross-references MUID:89025806
#accession        A31510
#molecule_type  protein
#residues         122-145 #label SNK
COMMENT          In mammals, several active peptides may be derived from the
               prohormone.
CLASSIFICATION   #superfamily natriuretic peptide A precursor
KEYWORDS         atrium; diuretic; hormone; natriuretic; osmoregulation
FEATURE          1-23      #domain signal sequence #status predicted #label SIG\
24-121          #domain propeptide #status predicted #label PRO\
122-145          #product atrial natriuretic peptide-24 #status
               experimental #label M24\
125-145          #product atrial natriuretic peptide-21 #status
               experimental #label M21\
125-141          #disulfide_bonds #status predicted
SUMMARY          #length 145 #molecular_weight 15934 #checksum 1892
Query Match     86.1%; Score 118; DB 2; Length 145;
Best Local Similarity 82.4%; Pred. No. 2.82e-13;
Matches 14; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Db 125 CFGSRIDRIGAQSGMGC 141
Qy 1 CFGGRMDRIGAQSGLCG 17

RESULT 13
ENTRY   S15821 #type complete
TITLE   ventricular natriuretic peptide - Japanese eel
ORGANISM #formal_name Anguilla japonica #common_name Japanese eel
DATE     04-Dec-1992 #sequence_revision 04-Dec-1992 #text_change
09-Dec-1994
ACCESSIONS S15821
REFERENCE   S15821
#authors    Takei, Y.; Takahashi, A.; Watanabe, T.X.; Nakajima, K.;
               Sakakibara, S.
#journal    FEBS Lett. (1991) 282:317-320
#title      A novel natriuretic peptide isolated from eel cardiac
               ventricles.
#cross-references MUID:91243821
#accession    S15821
#molecule_type protein
#residues     1-36 #label FEB
CLASSIFICATION #superfamily natriuretic peptide A precursor
SUMMARY        #length 36 #molecular_weight 3941 #checksum 388

Query Match     81.8%; Score 112; DB 2; Length 36;
Best Local Similarity 82.4%; Pred. No. 8.56e-12;
Matches 14; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Db 6 CFGTRMDRIGSWGLGC 22
Qy 1 CFGGRMDRIGAQSGLCG 17

```

```
RESULT 14
ENTRY   A33431      #type complete
TITLE   atrial natriuretic factor - Japanese eel
ORGANISM #formal_name Anguilla japonica #common_name Japanese eel
DATE    27-Feb-1990 #sequence_revision 27-Feb-1990 #text_change
        09-Dec-1994
ACCESSIONS A33431
REFERENCE  A33431
#authors   Takei, Y.; Takahashi, A.; Watanabe, T.X.; Nakajima, K.;
           Sakakibara, S.
#journal   Biochem. Biophys. Res. Commun. (1989) 164:537-543
#title     Amino acid sequence and relative biological activity of eel
           atrial natriuretic peptide.
#cross-references MUID:90026430
#accession  A33431
#status     preliminary
#molecule_type protein
#residues   1-27 #label TAK
CLASSIFICATION #superfamily natriuretic peptide A precursor
SUMMARY       #length 27 #molecular-weight 2792 #checksum 8900

Query Match      80.3%; Score 110; DB 2; Length 27;
Best Local Similarity 76.5%; Pred. No. 2.64e-11;
Matches 13; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Db      7 CFGGKLDRIQSYSLGDC 23
      ||||:||||: |||||
QY      1 CFGGRMDRIGAGSLGDC 17

RESULT 15
ENTRY   JC1081      #type complete
TITLE   brain natriuretic peptide - pig
ORGANISM #formal_name Sus scrofa domestica #common_name domestic pig
DATE    27-Aug-1995 #sequence_revision 19-Oct-1995 #text_change
        16-Feb-1997
ACCESSIONS JC1081
REFERENCE   JC1081
#authors   Chen, H.; Zhang, J.; Wang, Q.S.; Cui, H.; Tang, J.
           J. Fudan Univ. (Natur. Sci.) (1991) 30:413-416
#journal   Chemical synthesis and cloning of the porcine brain
           natriuretic gene.
#accession JC1081
#molecule_type DNA
#residues  1-27 #label CHE
#note      The translation of the start codon ATG is not given in
           this paper

GENETICS
#gene      bnp
CLASSIFICATION #superfamily natriuretic peptide A precursor
KEYWORDS     brain; natriuretic
SUMMARY       #length 27 #molecular-weight 3002 #checksum 9351

Query Match      77.4%; Score 106; DB 2; Length 27;
Best Local Similarity 76.5%; Pred. No. 2.46e-10;
Matches 13; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Db      5 CFGRRLDRIQSYSLGDC 21
      ||| |:||||: |||||
QY      1 CFGGRMDRIGAGSLGDC 17

Search completed: Wed Jun 16 13:14:53 1999
Job time : 20 secs.
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[M][A][T][R][I][U][R][E][T][I][C] (TM)

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MPsrch_pp protein - protein database search, using Smith-Waterman algorithm

Run on: Wed Jun 16 13:15:10 1999; MasPar time 2.30 Seconds
Tabular output not generated. 208.756 Million cell updates/sec

Title: >US-09-027-777B-1
Description: (1-17) from US09027777B.pep
Perfect Score: 137
Sequence: 1 CFGGRMDRIGAOSGLGC 17

Scoring table: PAM 150
Gap 15

Searched: 77977 seqs, 28268293 residues

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database: swiss-prot37
1:swissprot

Statistics: Mean 28.233; Variance 33.694; scale 0.838

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution..

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description	Pred. No.
1	137	100.0	149	1 ANF_CANFA	ATRIAL NATRIURETIC FAC	7.24e-21
2	137	100.0	150	1 ANF_PIG	ATRIAL NATRIURETIC FAC	7.24e-21
3	137	100.0	152	1 ANF_BOVIN	ATRIAL NATRIURETIC FAC	7.24e-21
4	137	100.0	153	1 ANF_HUMAN	ATRIAL NATRIURETIC FAC	7.24e-21
5	137	100.0	153	1 ANF_HORSE	ATRIAL NATRIURETIC FAC	7.24e-21
6	131	95.6	128	1 ANF_CAVPO	ATRIAL NATRIURETIC FAC	4.05e-19
7	128	93.4	152	1 ANF_MOUSE	ATRIAL NATRIURETIC FAC	2.98e-18
8	128	93.4	152	1 ANF_RAT	ATRIAL NATRIURETIC FAC	2.98e-18
9	128	93.4	153	1 ANF_RABIT	ATRIAL NATRIURETIC FAC	2.98e-18
10	118	86.1	30	1 ANF_RANRI	ATRIAL NATRIURETIC FAC	2.10e-15
11	118	86.1	145	1 ANF_RANCA	ATRIAL NATRIURETIC FAC	2.10e-15
12	112	81.8	36	1 ANFV_ANGJA	VENTRICULAR NATRIURETI	9.97e-14
13	110	80.3	27	1 ANFV_ANGJA	ATRIAL NATRIURETIC FAC	3.56e-13
14	106	77.4	103	1 ANF_BOVIN	BRAIN NATRIURETIC PEPT	4.45e-12
15	106	77.4	115	1 ANFC_TRISC	C-TYPE NATRIURETIC PEP	4.45e-12
16	106	77.4	115	1 ANFC_SCICA	C-TYPE NATRIURETIC PEP	4.45e-12
17	106	77.4	131	1 ANFB_PIG	BRAIN NATRIURETIC PEPT	4.45e-12
18	106	77.4	140	1 ANFB_CANFA	BRAIN NATRIURETIC PEPT	4.45e-12
19	104	75.9	22	1 ANFC_CHICK	C-TYPE NATRIURETIC PEP	1.55e-11
20	103	75.2	118	1 ANFD_RANCA	C-TYPE NATRIURETIC PEP	2.89e-11
21	103	75.2	134	1 ANFB_HUMAN	BRAIN NATRIURETIC PEPT	2.89e-11
22	103	75.2	135	1 ANFC_SQUAC	C-TYPE NATRIURETIC PEP	2.89e-11
23	101	73.7	126	1 ANFC_SHEEP	C-TYPE NATRIURETIC PEP	9.98e-11

24	101	73.7	126	1 ANFC_PIG	C-TYPE NATRIURETIC PEP	9.98e-11
25	101	73.7	126	1 ANFC_MOUSE	C-TYPE NATRIURETIC PEP	9.98e-11
26	101	73.7	126	1 ANFC_HUMAN	C-TYPE NATRIURETIC PEP	9.98e-11
27	101	73.7	126	1 ANFC_BOVIN	C-TYPE NATRIURETIC PEP	9.98e-11
28	101	73.7	126	1 ANFC_RAT	C-TYPE NATRIURETIC PEP	9.98e-11
29	101	73.7	129	1 ANFC_RANCA	C-TYPE NATRIURETIC PEP	9.98e-11
30	100	73.0	131	1 ANFC_ANGJA	C-TYPE NATRIURETIC PEP	1.85e-10
31	100	73.0	140	1 ANFC_CHICK	ATRIAL NATRIURETIC FAC	1.85e-10
32	90	65.7	121	1 ANFB_RAT	BRAIN NATRIURETIC PEPT	7.70e-08
33	86	62.8	121	1 ANFB_MOUSE	BRAIN NATRIURETIC PEPT	8.00e-07
34	79	57.7	38	1 DNP_DENAN	NATRIURETIC PEPTIDE (D	4.28e-05
35	70	51.1	683	1 EBL_TREPA	ELONGATION FACTOR G (E	5.56e-03
36	65	47.4	699	1 EFG_RICPR	ELONGATION FACTOR G (E	7.16e-02
37	65	47.4	701	1 EFG_MYCLE	ELONGATION FACTOR G (E	7.16e-02
38	65	47.4	701	1 EFG_MYCTU	ELONGATION FACTOR G (E	7.16e-02
39	64	46.7	788	1 EFGC_SOVEN	ELONGATION FACTOR G, C	1.18e-01
40	63	46.0	1124	1 PHYL_TOBAC	PHYTOCHROME AL	1.92e-01
41	62	45.3	819	1 EFG2_YEAST	ELONGATION FACTOR G, M	3.13e-01
42	61	44.5	302	1 YGBJ_ECOLI	HYPOTHETICAL 30.8 KD P	5.06e-01
43	60	43.8	404	1 YK33_YEAST	HYPOTHETICAL 46.5 KD P	8.14e-01
44	60	43.8	701	1 EFG_MICLU	ELONGATION FACTOR G (E	8.14e-01
45	60	43.8	846	1 VAV_HUMAN	VAV PROTO-ONCOGENE.	8.14e-01

ALIGNMENTS

RESULT 1
ID ANF_CANFA STANDARD; PRT; 149 AA.
AC P07499;
DT 01-APR-1988 (REL. 07, CREATED)
DT 01-APR-1988 (REL. 07, LAST SEQUENCE UPDATE)
DT 01-OCT-1996 (REL. 34, LAST ANNOTATION UPDATE)
DE ATRIAL NATRIURETIC FACTOR PRECURSOR (ANF) (ATRIAL NATRIURETIC PEPTIDE)
DE (ANP) (PREPRONATRIODILATIN).
GN NPFA.
OS CANIS FAMILIARIS (DOG).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA;
OC CARNIVORA; FISSIPEDIA; CANIDAE; CANIS.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE: 86076957.
RA OIKAWA S., IMAI M., INUZUKA C., TAWARAGI Y., NAKAZATO H., MATSUO H.;
RT "Structure of dog and rabbit precursors of atrial natriuretic
polypeptides deduced from nucleotide sequence of cloned cDNA";
RL BIOCHEM. BIOPHYS. RES. COMMUN. 132:892-899(1985).
CC -1- FUNCTION: ATRIAL NATRIURETIC FACTOR (ANF) IS A POTENT VASOACTIVE
SUBSTANCE, SYNTHESIZED IN MAMMALIAN ATRIA AND IS THOUGHT TO PLAY A
KEY ROLE IN CARDIOVASCULAR HOMEOSTASIS. HAS A COMP-STIMULATING
ACTIVITY.
CC -1- A DISULFIDE BOND IS REQUIRED FOR FULL ACTIVITY OF ATRIOPEPTINS.
CC -1- SIMILARITY: BELONGS TO THE NATRIURETIC PEPTIDES FAMILY.
CC
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CC EMBL: M12045; G163901;
CC PIR: A25302; AWDG.
CC PROSITE: PS00263; NATRIURETIC_PEPTIDE; 1.
CC PAM: P000212; ANP; 1.
CC VASOACTIVE; SIGNAL.
FT SIGNAL 1 23
FT PEPTIDE 122 149 ATRIAL NATRIURETIC PEPTIDE, ALPHA (ANP).
FT DISULFID 128 144
SQ SEQUENCE 149 AA; 15819 MW; D4F3A6CF CRC32;

Query Match 100.0%; Score 137; DB 1; Length 149;
Best Local Similarity 100.0%; Pred. No. 7.24e-21;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 128 CFGGRMDRIGASGLGC 144
 |||||||
 QY 1 CFGGRMDRIGASGLGC 17

RESULT 2
 ID ANF_PIG STANDARD; PRT: 150 AA.
 AC P24259;
 DT 01-MAR-1992 (REL. 21, CREATED)
 DT 01-MAR-1992 (REL. 21, LAST SEQUENCE UPDATE)
 DT 01-OCT-1996 (REL. 34, LAST ANNOTATION UPDATE)
 DE ATRIAL NATRIURETIC FACTOR PRECURSOR (ANF) (ATRIAL NATRIURETIC PEPTIDE)
 DE (ANP) (PREPRONATRIODILATIN).
 GN NPFA.
 OS SUS SCROFA (PIG).
 OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA;
 OC ARTIODACTYLA; SUIFORMES; SUINA; SUIDAE; SUS.
 RN [1]
 RP SEQUENCE FROM N.A.
 RX TISSUE-HEART RIGHT ATRIUM;
 RX MEDLINE; 91067478.
 RA MAERGERT H.J., APPELHANS H., GASSEN H.G., FORSSMANN W.G.;
 RT "Nucleotide sequence of a porcine prepro atrial natriuretic peptide
 (ANP) cDNA.";
 RL NUCLEIC ACIDS RES. 18:6704-6704(1990).
 RN [2]
 RP SEQUENCE OF 25-150.
 RC TISSUE-HEART RIGHT ATRIUM;
 RX MEDLINE; 85124561.
 RA FORSSMANN W.G., BIRR C., CARLQUIST M., CHRISTMANN M., FINKE R.,
 RA HENSCHEN A., HOCK D., KIRCHHEIM H., KREYE V., LOTTSCHEICH F., METZ J.,
 RA MUTT V., REINECKE M.;
 RT "The atricular myocytes of the heart constitute an endocrine
 organ. Characterization of a porcine cardiac peptide hormone,
 cardiodilatin-126.";
 RL CELL TISSUE RES. 238:425-430(1984).
 CC -!- FUNCTION: ATRIAL NATRIURETIC FACTOR (ANF) IS A POTENT VASOACTIVE
 CC SUBSTANCE SYNTHESIZED IN MAMMALIAN ATRIA AND IS THOUGHT TO PLAY A
 CC KEY ROLE IN CARDIOVASCULAR HOMEOSTASIS. HAS A CGMP-STIMULATING
 CC ACTIVITY.
 CC -!- A DISULFIDE BOND IS REQUIRED FOR FULL ACTIVITY OF ATRIOPEPTINS.
 CC -!- SIMILARITY: BELONGS TO THE NATRIURETIC PEPTIDES FAMILY.
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 CC
 CC EMBL: X54669; GI884;
 CC PIR: S13107; S13107.
 CC PROSITE; PS00263; NATRIURETIC_PEPTIDE; 1.
 CC PFAM; PF00212; ANP; 1.
 CC KW VASOACTIVE; SIGNAL.
 CC SIGNAL 1 24
 CC PEPTIDE 25 54
 CC CARDIODILATIN-RELATED PEPTIDE (CDP)
 CC (BY SIMILARITY)
 CC
 CC PEPTIDE 123 150
 CC DISULFID 129 145
 CC BY SIMILARITY.
 CC SEQUENCE 150 AA; 16351 MW; 4FF67B94 CRC32;
 CC
 CC Query Match 100.0%; Score 137; DB 1; Length 150;
 CC Best Local Similarity 100.0%; Pred. No. 7.24e-21;
 CC Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 129 CFGGRMDRIGASGLGC 145
 |||||||
 QY 1 CFGGRMDRIGASGLGC 17

RESULT 3
 ID ANF_BOVIN STANDARD; PRT: 152 AA.
 AC P07501;
 DT 01-APR-1988 (REL. 07, CREATED)
 DT 01-MAR-1989 (REL. 10, LAST SEQUENCE UPDATE)
 DT 01-OCT-1996 (REL. 34, LAST ANNOTATION UPDATE)
 DE ATRIAL NATRIURETIC FACTOR PRECURSOR (ANF) (ATRIAL NATRIURETIC PEPTIDE)
 DE (ANP) (PREPRONATRIODILATIN).
 GN NPFA.
 OS BOS TAURUS (BOVINE).
 OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA;
 OC ARTIODACTYLA; RUMINANTIA; PECORA; BOVIDAE; BOVINAE; BOS.
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE; 86215205.
 RA VLASUK G.P., MILLER J., BENGEN G.H., LEWICKI J.A.;
 RT "Structure and analysis of the bovine atrial natriuretic peptide
 precursor gene.";
 RL BIOCHEM. BIOPHYS. RES. COMMUN. 136:396-403(1986).
 RN [2]
 RP SEQUENCE OF 123-150.
 RX MEDLINE; 86173941.
 RA ONG H., MCNICOLL N., LAZURE C., SEIDAH N., CHRETIEN M., CANTIN M.,
 RA DE LEAN A.;
 RT "Purification and sequence determination of bovine atrial natriuretic
 factor.";
 RL LIFE SCI. 38:1309-1315(1986).
 CC -!- FUNCTION: ATRIAL NATRIURETIC FACTOR (ANF) IS A POTENT VASOACTIVE
 CC SUBSTANCE SYNTHESIZED IN MAMMALIAN ATRIA AND IS THOUGHT TO PLAY A
 CC KEY ROLE IN CARDIOVASCULAR HOMEOSTASIS. HAS A CGMP-STIMULATING
 CC ACTIVITY.
 CC -!- A DISULFIDE BOND IS REQUIRED FOR FULL ACTIVITY OF ATRIOPEPTINS.
 CC -!- SIMILARITY: BELONGS TO THE NATRIURETIC PEPTIDES FAMILY.
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 CC
 CC EMBL: M13145; G162666;
 CC PIR: A24247; AWBO.
 CC PROSITE; PS00263; NATRIURETIC_PEPTIDE; 1.
 CC PFAM; PF00212; ANP; 1.
 CC KW VASOACTIVE; SIGNAL.
 CC SIGNAL 1 24
 CC PEPTIDE 123 150
 CC DISULFID 129 145
 CC ATRIAL NATRIURETIC PEPTIDE, ALPHA (ANP).
 CC SEQUENCE 152 AA; 16518 MW; CF200882 CRC32;
 CC
 CC Query Match 100.0%; Score 137; DB 1; Length 152;
 CC Best Local Similarity 100.0%; Pred. No. 7.24e-21;
 CC Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 129 CFGGRMDRIGASGLGC 145
 |||||||
 QY 1 CFGGRMDRIGASGLGC 17

RESULT 4
 ID ANF_HUMAN STANDARD; PRT: 153 AA.
 AC P01160;
 DT 21-JUL-1986 (REL. 01, CREATED)
 DT 13-AUG-1987 (REL. 05, LAST SEQUENCE UPDATE)
 DT 15-DEC-1998 (REL. 37, LAST ANNOTATION UPDATE)
 DE ATRIAL NATRIURETIC FACTOR PRECURSOR (ANF) (ATRIAL NATRIURETIC PEPTIDE)
 DE (ANP) (PREPRONATRIODILATIN).
 GN NPFA OR PND.
 OS HOMO SAPIENS (HUMAN).
 OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA;
 OC PRIMATES; CATARRHINI; HOMINIDAE; HOMO.

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DR EMBL: X58563; G1009; -
 DR PIR: S14873; S14873.
 DR PROSITE: PS00263; NATRIURETIC_PEPTIDE; 1.
 DR PFAM: PF00212; ANP; 1.
 KW VASOACTIVE; SIGNAL. 25
 FT SIGNAL 1 POTENTIAL.
 FT PEPTIDE 124 151 ATRIAL NATRIURETIC PEPTIDE, ALPHA (ANP).
 FT DISULFID 130 146 BY SIMILARITY.
 SQ SEQUENCE 153 AA: 16825 MW: 252544 CRC32:

Query Match 100.0%; Score 137; DB 1; Length 153;
 Best Local Similarity 100.0%; Pred. No. 7.24e-21;
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 130 CFGGRMDRIGAQSGLGC 146
 QY 1 CFGGRMDRIGAQSGLGC 17

RESULT 6
 ID ANF_CAVPO STANDARD; PRT: 128 AA.
 AC P27196;
 DT 01-AUG-1992 (REL. 23, CREATED)
 DT 01-AUG-1992 (REL. 23, LAST SEQUENCE UPDATE)
 DT 01-OCT-1996 (REL. 34, LAST ANNOTATION UPDATE)
 DE ATRIAL NATRIURETIC FACTOR PRECURSOR (ANP) (ATRIAL NATRIURETIC PEPTIDE)
 DE (ANP) (PREPRONATRIODILATIN) (FRAGMENT).
 GN NPFA.
 OS CAVIA PORCELLUS (GUINEA PIG).
 OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA;
 OC RODENTIA; HYSTRICOGNATHI; CAVIIDAE; CAVIA.
 RN [1]

RP TISSUE=HEART ATRIUM;
 RA MAEGERT H.J.; HANKE M.; SCHMEDING G.; TEUTEBERG K.,
 RA SCHULZ-KNAPPE P.; FORSSMANN W.G.;
 RL SUBMITTED (MAR-1991) TO EMBL/GENBANK/DBJ DATA BANKS.
 CC -!- FUNCTION: ATRIAL NATRIURETIC FACTOR (ANP) IS A POTENT VASOACTIVE
 CC SUBSTANCE SYNTHESIZED IN MAMMALIAN ATRIA AND IS THOUGHT TO PLAY A
 CC KEY ROLE IN CARDIOVASCULAR HOMEOSTASIS. HAS A CGMP-STIMULATING
 CC ACTIVITY.
 CC -!- DEVELOPMENTAL STAGE: ADULT.
 CC -!- A DISULFIDE BOND IS REQUIRED FOR FULL ACTIVITY OF ATRIOPEPTINS.
 CC -!- SIMILARITY: BELONGS TO THE NATRIURETIC PEPTIDES FAMILY.

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DR EMBL: X58562; G49544; -
 DR PIR: S14872; S14872.
 DR PROSITE: PS00263; NATRIURETIC_PEPTIDE; 1.
 DR PFAM: PF00212; ANP; 1.
 KW VASOACTIVE.
 FT NON_TER 1 1
 FT PEPTIDE 1 30 CARDIODILATIN-RELATED PEPTIDE (CDP).
 FT PEPTIDE 99 126 ATRIAL NATRIURETIC PEPTIDE, ALPHA (ANP).
 FT DISULFID 105 121 BY SIMILARITY.
 SQ SEQUENCE 128 AA: 13966 MW: 252552 CRC32:

Query Match 95.6%; Score 131; DB 1; Length 128;
 Best Local Similarity 94.1%; Pred. No. 4.05e-19;
 Matches 16; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Db 105 CFGGRMDRIGAQSGLGC 121
 QY 1 CFGGRMDRIGAQSGLGC 17

RESULT 7
 ID ANF_MOUSE STANDARD; PRT: 152 AA.
 AC P05125;
 DT 13-AUG-1987 (REL. 05, CREATED)
 DT 13-AUG-1987 (REL. 05, LAST SEQUENCE UPDATE)
 DT 01-OCT-1996 (REL. 34, LAST ANNOTATION UPDATE)
 DE ATRIAL NATRIURETIC FACTOR PRECURSOR (ANP) (ATRIAL NATRIURETIC PEPTIDE)
 DE (ANP) (PREPRONATRIODILATIN).
 GN NPFA OR PND.
 OS MUS MUSCULUS (MOUSE).
 OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA;
 OC RODENTIA; SCIUROGNATHI; MURIDAE; MURINAE; MUS.
 RN [1]

RP SEQUENCE FROM N.A.
 RX MEDLINE; 85065766.
 RA SEIDMAN C.E.; BLOCH K.D.; KLEIN K.A.; SMITH J.A.; SEIDMAN J.G.;
 RT "Nucleotide sequences of the human and mouse atrial natriuretic
 RT factor genes".
 RL SCIENCE 226:1206-1209(1984).

CC -!- FUNCTION: ATRIAL NATRIURETIC FACTOR (ANP) IS A POTENT VASOACTIVE
 CC SUBSTANCE SYNTHESIZED IN MAMMALIAN ATRIA AND IS THOUGHT TO PLAY A
 CC KEY ROLE IN CARDIOVASCULAR HOMEOSTASIS. HAS A CGMP-STIMULATING
 CC ACTIVITY.
 CC -!- A DISULFIDE BOND IS REQUIRED FOR FULL ACTIVITY OF ATRIOPEPTINS.
 CC -!- SIMILARITY: BELONGS TO THE NATRIURETIC PEPTIDES FAMILY.

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DR EMBL: K02781; G387099; -
 DR PIR: A29370; AWMS.
 DR MGD: MGI:97367; NPFA.
 DR PROSITE: PS00263; NATRIURETIC_PEPTIDE; 1.
 DR PFAM: PF00212; ANP; 1.
 KW VASOACTIVE; SIGNAL.
 FT SIGNAL 1 24
 FT PEPTIDE 126 149 AURICULIN A (BY SIMILARITY).
 FT PEPTIDE 126 150 AURICULIN B (BY SIMILARITY).
 FT PEPTIDE 127 149 ATRIOPEPTIN I (BY SIMILARITY).
 FT PEPTIDE 127 147 ATRIOPEPTIN II (BY SIMILARITY).
 FT DISULFID 129 145 BY SIMILARITY.
 SQ SEQUENCE 152 AA: 16545 MW: 5163823 CRC32:

Query Match 93.4%; Score 128; DB 1; Length 152;
 Best Local Similarity 94.1%; Pred. No. 2.98e-18;
 Matches 16; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Db 129 CFGGRMDRIGAQSGLGC 145
 QY 1 CFGGRMDRIGAQSGLGC 17

RESULT 8
 ID ANF_RAT STANDARD; PRT: 152 AA.
 AC P01161;
 DT 21-JUL-1986 (REL. 01, CREATED)
 DT 21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)
 DT 15-DEC-1998 (REL. 37, LAST ANNOTATION UPDATE)
 DE ATRIAL NATRIURETIC FACTOR PRECURSOR (ANP) (ATRIAL NATRIURETIC PEPTIDE)
 DE (ANP) (PREPRONATRIODILATIN) (CONTAINS: AURICULINS; ATRIOPEPTINS).
 GN NPFA.
 OS RATTUS NORVEGICUS (RAT).

OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA;
 OD RODENTIA; SCIUROGNATHI; MURIDAE; MURINAE; RATTUS.
 RP [1]
 RX SEQUENCE FROM N.A.
 RA MEDLINE: 84219797.
 RA YAMANAKA M., GREENBERG B., JOHNSON L., SEILHAWER J.J., BREWER M.,
 RA FRIEDEMANN T., MILLER J., ATLAS S.A., LARAGH J., LEWICKI J.,
 RA FIDDES J.C.;
 RT "Cloning and sequence analysis of the cDNA for the rat atrial
 RT natriuretic factor precursor.";
 RL NATURE 309:719-722(1984).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE: 84219798.
 RA HAKI M., TAKAYANAGI R., MISONO K.S., PANDEY K.N., TIBBETTS C.,
 RA INAGAMI T.;
 RT "Structure of rat atrial natriuretic factor precursor deduced from
 RT cDNA sequence.";
 RL NATURE 309:722-724(1984).
 RN [3]
 RP SEQUENCE FROM N.A.
 RX MEDLINE: 84250178.
 RA SEIDMAN C.E., DUBY A.D., CHOI E., GRAHAM R.M., HABER E., HOMCY C.,
 RA SMITH J.A., SEIDMAN J.G.;
 RT "The structure of rat preproatrial natriuretic factor as defined by a
 RT complementary DNA clone.";
 RL SCIENCE 225:324-326(1984).
 RN [4]
 RP SEQUENCE FROM N.A.
 RX MEDLINE: 85061500.
 RA KAKAWA K., TAWARAGI Y., OIKAWA S., MIZUNO A., SAKURAGAWA Y.,
 RA NAKAZATO H., FUKUDA A., MINAMINO N., MATSUO H.;
 RT "Identification of rat gamma atrial natriuretic polypeptide and
 RT characterization of the cDNA encoding its precursor.";
 RL NATURE 312:152-155(1984).
 RN [5]
 RP SEQUENCE FROM N.A.
 RX MEDLINE: 85182558.
 RA ARGENTIN S., NEMER M., DROUIN J., SCOTT G.K., KENNEDY B.P.,
 RA DAVIES P.L.;
 RT "The gene for rat atrial natriuretic factor.";
 RL J. BIOL. CHEM. 260:4568-4571(1985).
 RN [6]
 RP SEQUENCE FROM N.A.
 RX MEDLINE: 85038509.
 RA ZIVIN R.A., CONDERA J.H., DIXON R.A.F., SEIDAH N.G., CHRETIEN M.,
 RA NEMER M., CHAMBERLAND M., DROUIN J.;
 RT "Molecular cloning and characterization of DNA sequences encoding rat
 RT and human atrial natriuretic factors.";
 RL PROC. NATL. ACAD. SCI. U.S.A. 81:6325-6329(1984).
 RN [7]
 RP SEQUENCE FROM N.A.
 RX MEDLINE: 88109092.
 RA FLYNN T.G.;
 RT "The elucidation of the structure of atrial natriuretic factor, a new
 RT peptide hormone.";
 RL CAN. J. PHYSIOL. PHARMACOL. 65:2013-2020(1987).
 RN [8]
 RP SEQUENCE OF 38-152 FROM N.A.
 RX MEDLINE: 87175636.
 RA GARDNER D.G., VLASUK G.P., BAXTER J.D., FIDDES J.C., LEWICKI J.A.;
 RT "Identification of atrial natriuretic factor gene transcripts in the
 RT central nervous system of the rat.";
 RL PROC. NATL. ACAD. SCI. U.S.A. 84:2175-2179(1987).
 RN [9]
 RP AURICULINS, SEQUENCE, AND SYNTHESIS OF 126-149.
 RX MEDLINE: 84219796.
 RA ATLAS S.A., KLEINERT H.D., CAMARGO M.J., JANUSZEWICZ A., SEALEY J.E.,
 RA LARAGH J.H., SCHILLING J.W., LEWICKI J.A., JOHNSON L.K., MACK T.;
 RT "Purification, sequencing and synthesis of natriuretic and vasoactive
 RT rat atrial peptide.";
 RL NATURE 309:717-719(1984).
 RN [10]

RP SEQUENCE OF 127-149, AND SYNTHESIS.
 RX MEDLINE: 84097513.
 RA CURRIE M.G., GELLER D.M., COLE B.R., SIEGEL N.R., FOK K.F.,
 RA ADAMS S.P., EUBANKS S.R., GALLUPPI G.R., NEEDLEMAN P.;
 RT "Purification and sequence analysis of bioactive atrial peptides
 RT (atriopeptins).";
 RL SCIENCE 223:67-69(1984).
 RN [11]
 RP SEQUENCE OF 118-150.
 RX MEDLINE: 84194062.
 RA SEIDAH N.G., LAZURE C., CHRETIEN M., THIBAUT G., GARCIA R.,
 RA CANTIN M., GENEST J., NUTT R.F., BRADY S.F., LYLE T.A., PALEVEDA W.J.,
 RA COLTON C.D., CICCAREONE T.M., WEBER D.F.;
 RT "Amino acid sequence of homologous rat atrial peptides: natriuretic
 RT activity of native and synthetic forms.";
 RL PROC. NATL. ACAD. SCI. U.S.A. 81:2640-2644(1984).
 RN [12]
 RP SEQUENCE OF 25-38.
 RX MEDLINE: 88203350.
 RA THIBAUT G., MURTHY K.K., GUTKOWSKA J., SEIDAH N.G., LAZURE C.,
 RA CHRETIEN M., CANTIN M.;
 RT "NH2-terminal fragment of rat pro-atrial natriuretic factor in the
 RT circulation: identification, radioimmunoassay and half-life.";
 RL PEPTIDES 9:47-53(1988).
 CC -I- FUNCTION: ATRIAL NATRIURETIC FACTOR (ANF) IS A POTENT VASOACTIVE
 CC SUBSTANCE SYNTHESIZED IN MAMMALIAN ATRIA AND IS THOUGHT TO PLAY A
 CC KEY ROLE IN CARDIOVASCULAR HOMEOSTASIS. HAS A CGMP-STIMULATING
 CC ACTIVITY.
 CC -I- A DISULFIDE BOND IS REQUIRED FOR FULL ACTIVITY OF ATRIOPEPTINS.
 CC -I- SIMILARITY: BELONGS TO THE NATRIURETIC PEPTIDES FAMILY.
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 CC -----
 DR EMBL: M15868; G202904;
 DR EMBL: X00665; G55712;
 DR EMBL: K02062; G202900;
 DR EMBL: X01118; G55717;
 DR EMBL: M27498; G202906;
 DR PIR: A22570; AWRT.
 DR PIR: A44190; A44190.
 DR PROSITE: PS00263; NATRIURETIC_PEPTIDE; 1.
 DR PFAM: PF00212; ANP; 1.
 KW VASOACTIVE; SIGNAL.
 FT SIGNAL 1 24
 FT PEPTIDE 126 149 AURICULIN A.
 FT PEPTIDE 126 150 AURICULIN B.
 FT PEPTIDE 127 147 ATRIOPEPTIN I.
 FT PEPTIDE 127 149 ATRIOPEPTIN II.
 FT PEPTIDE 127 150 ATRIOPEPTIN III.
 FT DISULFID 129 145
 SQ SEQUENCE 152 AA; 16556 MW; 2D424B75 CRC32;
 Query Match 93.48; Score 128; DB 1; Length 152;
 Best Local Similarity 94.18; Pred. No. 2.98e-18;
 Matches 16; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 Db 129 CFGGRIDRIGAQSGLCG 145
 QY 1 CFGGRIDRIGAQSGLCG 17
 RESULT 9
 ID ANF RABIT STANDARD; PRT; 153 AA.
 AC P07500;
 DT 01-APR-1988 (REL. 07, CREATED)
 DT 01-APR-1988 (REL. 07, LAST SEQUENCE UPDATE)
 DT 01-OCT-1996 (REL. 34, LAST ANNOTATION UPDATE)

DE ATRIAL NATRIURETIC FACTOR PRECURSOR (ANF) (ATRIAL NATRIURETIC PEPTIDE)
DE (ANP) (PREPRONATRIODILATIN).
GN NPPA.
OS OXYCTOLAGUS CUNICULUS (RABBIT).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA;
OC LAGOMORPHA; LEPORIDAE; ORYCTOLAGUS.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE; 86076957.
RA OKAWA S., IMAI M., INUZUKA C., TAWARAGI Y., NAKAZATO H., MATSUO H.;
RT "Structure of dog and rabbit precursors of atrial natriuretic
polypeptides deduced from nucleotide sequence of cloned cDNA.";
RL BIOCHEM. BIOPHYS. RES. COMMUN. 132:892-899(1985).
CC -!- FUNCTION: ATRIAL NATRIURETIC FACTOR (ANF) IS A POTENT VASOACTIVE
SUBSTANCE SYNTHESIZED IN MAMMALIAN ATRIA AND IS THOUGHT TO PLAY A
KEY ROLE IN CARDIOVASCULAR HOMEOSTASIS. HAS A CGMP-STIMULATING
ACTIVITY.
CC -!- A DISULFIDE BOND IS REQUIRED FOR FULL ACTIVITY OF ATRIOPEPTINS.
CC -!- SIMILARITY: BELONGS TO THE NATRIURETIC PEPTIDES FAMILY.
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DR EMBL; M12046; G164771; .
DR PIR; B25302; AWRB.
DR PROSITE; PS00263; NATRIURETIC_PEPTIDE; 1.
DR PFAM; PF00212; ANP; 1.
KW VASOACTIVE; SIGNAL.
FT SIGNAL 1 25
FT PEPTIDE 124 151 ATRIAL NATRIURETIC PEPTIDE, ALPHA (ANP).
FT DISULFID 130 146
FT SEQUENCE 153 AA; 16943 MW; 1FA4FB42 CRC32;
Query Match 93.4%; Score 128; DB 1; Length 153;
Best Local Similarity 94.1%; Pred. No. 2.98e-18;
Matches 16; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
Db 130 CFGGRMDRIGAQSGLGC 146
QY 1 CFGGRMDRIGAQSGLGC 17
|||||:|||||
RESULT 10
ID ANF_RANRI STANDARD; PRT; 30 AA.
AC P09196;
DT 01-MAR-1989 (REL. 10, CREATED)
DT 01-MAR-1989 (REL. 10, LAST SEQUENCE UPDATE)
DT 01-FEB-1995 (REL. 31, LAST ANNOTATION UPDATE)
DE ATRIAL NATRIURETIC FACTOR (ANF) (ATRIAL NATRIURETIC PEPTIDE) (ANP).
OS RANA RADIBUNDA (LAUGHING FROG) (MARSH FROG).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; AMPHIBIA; BATRACHIA; ANURA;
OC NEOBATRACHIA; RANOIDEA; RANIDAE; RANINAE; RANA.
RN [1]
RP SEQUENCE.
RX TISSUE=HEART ATRIUM;
RX MEDLINE; 89003705.
RA LAZURE C., ONG H., MCNICOLL N., NETCHITAYLO P., CHRETIEN M.,
RA DE LEAN A., VAUDRY H.;
RT "The amino acid sequences of frog heart atrial natriuretic-like
peptide and mammalian ANP are closely related.";
RL FEBS LETT. 238:300-306(1988).
CC -!- FUNCTION: VASOACTIVE ACTIVITY. HAS A CGMP-STIMULATING ACTIVITY.
CC -!- SIMILARITY: BELONGS TO THE NATRIURETIC PEPTIDES FAMILY.
DR PIR; S01657; S01657.
DR PROSITE; PS00263; NATRIURETIC_PEPTIDE; 1.
DR PFAM; PF00212; ANP; 1.
KW VASOACTIVE.
FT DISULFID 11 27

SQ SEQUENCE 30 AA; 3263 MW; 14A325F7 CRC32;
Query Match 86.1%; Score 118; DB 1; Length 30;
Best Local Similarity 82.4%; Pred. No. 2.10e-15;
Matches 14; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
Db 11 CFGSRIDRIGAQSGLGC 27
QY 1 CFGGRMDRIGAQSGLGC 17
|||||:|||||
RESULT 11
ID ANF_RANCA STANDARD; PRT; 145 AA.
AC P18909;
DT 01-NOV-1990 (REL. 16, CREATED)
DT 01-MAR-1992 (REL. 21, LAST SEQUENCE UPDATE)
DT 01-FEB-1995 (REL. 31, LAST ANNOTATION UPDATE)
DE ATRIAL NATRIURETIC FACTOR PRECURSOR (ANF) (ATRIAL NATRIURETIC PEPTIDE)
DE (ANP).
OS RANA CATESBEIANA (BULL FROG).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; AMPHIBIA; BATRACHIA; ANURA;
OC NEOBATRACHIA; RANOIDEA; RANIDAE; RANINAE; RANA.
RN [1]
RP SEQUENCE FROM N.A.
RA KOUJIMA M.;
RL SUBMITTED (XXX-1992) TO EMBL/GENBANK/DBJ DATA BANKS.
RN [2]
RP SEQUENCE OF 122-145.
RC TISSUE=HEART;
RX MEDLINE; 89025806.
RA SAKATA J., KANGAWA K., MATSUO H.;
RT "Identification of new atrial natriuretic peptides in frog heart.";
RL BIOCHEM. BIOPHYS. RES. COMMUN. 155:1338-1345(1988).
CC -!- FUNCTION: VASOACTIVE ACTIVITY. HAS A CGMP-STIMULATING ACTIVITY.
CC -!- SIMILARITY: BELONGS TO THE NATRIURETIC PEPTIDES FAMILY.
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CC -----
DR EMBL; D01043; D1001314; .
DR PIR; A31510; A31510.
DR PIR; JQ0947; JQ0947.
DR PROSITE; PS00263; NATRIURETIC_PEPTIDE; 1.
DR PFAM; PF00212; ANP; 1.
KW VASOACTIVE; SIGNAL.
FT SIGNAL 1 23 POTENTIAL.
FT PEPTIDE 122 145 ATRIAL NATRIURETIC FACTOR.
FT DISULFID 125 141
FT SEQUENCE 145 AA; 15934 MW; 6A1FA352 CRC32;
Query Match 86.1%; Score 118; DB 1; Length 145;
Best Local Similarity 82.4%; Pred. No. 2.10e-15;
Matches 14; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
Db 125 CFGSRIDRIGAQSGLGC 141
QY 1 CFGGRMDRIGAQSGLGC 17
|||||:|||||
RESULT 12
ID ANFV_NGJA STANDARD; PRT; 36 AA.
AC P22642;
DT 01-AUG-1991 (REL. 19, CREATED)
DT 01-AUG-1991 (REL. 19, LAST SEQUENCE UPDATE)
DT 15-JUL-1998 (REL. 36, LAST ANNOTATION UPDATE)
DE VENTRICULAR NATRIURETIC PEPTIDE (VNP).
OS ANGUILLA JAPONICA (JAPANESE EEL).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; ACTINOPTERYGII; NEOPTERYGII;

OC TELEOSTEI; ANGUILLIFORMES; ANGUILLIDAE; ANGUILLA.
 RN [1]
 RP SEQUENCE.
 RX MEDLINE: 91243821.
 RA TAKEI Y., TAKAHASHI A., WATANABE T.X., NAKAJIMA K., SAKAKIBARA S.;
 RT "A novel natriuretic peptide isolated from eel cardiac ventricles."
 RL FEBS LETT. 282:317-320(1991).
 CC -!- FUNCTION: EXHIBITS NATRIURETIC AND VASODEPRESSOR ACTIVITY.
 CC -!- SIMILARITY: BELONGS TO THE NATRIURETIC PEPTIDES FAMILY.
 DR PIR: S15821; S15821.
 DR PROSITE: PS00263; NATRIURETIC_PEPTIDE; 1.
 DR PFAM: PF00212; ANP; 1.
 KW VASOACTIVE.
 FT DISULFID 6 22
 SQ SEQUENCE 36 AA; 3941 MW; B3E8D338 CRC32;
 Query Match 81.8%; Score 112; DB 1; Length 36;
 Best Local Similarity 82.4%; Pred. No. 9.97e-14;
 Matches 14; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
 Db 6 CFCGRMDRIGVSLGCG 22
 QY 1 CFCGRMDRIGVSLGCG 17
 RESULT 13
 ID ANF_ANGJA STANDARD; PRT; 27 AA.
 AC P18144;
 DT 01-NOV-1990 (REL. 16, LAST SEQUENCE UPDATE)
 DT 01-NOV-1990 (REL. 16, LAST SEQUENCE UPDATE)
 DT 15-JUL-1998 (REL. 36, LAST ANNOTATION UPDATE)
 DE ATRIAL NATRIURETIC FACTOR (ANF) (ATRIAL NATRIURETIC PEPTIDE) (ANP).
 OS ANGUILLA JAPONICA (JAPANESE EEL).
 OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; ACTINOPTERYGII; NEOPTERYGII;
 OC TELEOSTEI; ANGUILLIFORMES; ANGUILLIDAE; ANGUILLA.
 RN [1]
 RP SEQUENCE.
 RC TISSUE-HEART ATRIUM;
 RX MEDLINE: 90026430.
 RA TAKEI Y., TAKAHASHI A., WATANABE T.X., NAKAJIMA K., SAKAKIBARA S.;
 RT "Amino acid sequence and relative biological activity of eel atrial
 natriuretic peptide."
 RL BIOCHEM. BIOPHYS. RES. COMMUN. 164:537-543(1989).
 CC -!- FUNCTION: EXHIBITS NATRIURETIC AND VASODEPRESSOR ACTIVITY. HAS A
 CGMP-STIMULATING ACTIVITY.
 CC -!- SIMILARITY: BELONGS TO THE NATRIURETIC PEPTIDES FAMILY.
 DR PIR: A33431; A33431.
 DR PROSITE: PS00263; NATRIURETIC_PEPTIDE; 1.
 DR PFAM: PF00212; ANP; 1.
 KW VASOACTIVE.
 FT DISULFID 7 23
 SQ SEQUENCE 27 AA; 2792 MW; CA151EFA CRC32;
 Query Match 80.3%; Score 110; DB 1; Length 27;
 Best Local Similarity 76.5%; Pred. No. 3.56e-13;
 Matches 13; Conservative 3; Mismatches 1; Indels 0; Gaps 0;
 Db 7 CFCGKLDRTGVSGLGCG 23
 QY 1 CFCGRMDRIGVSLGCG 17
 RESULT 14
 ID ANFB_BOVIN STANDARD; PRT; 103 AA.
 AC P13204;
 DT 01-JAN-1990 (REL. 13, CREATED)
 DT 01-DEC-1992 (REL. 24, LAST SEQUENCE UPDATE)
 DT 01-OCT-1996 (REL. 34, LAST ANNOTATION UPDATE)
 DE BRAIN NATRIURETIC PEPTIDE PRECURSOR (BNP) (ALDOSTERONE SECRETION
 INHIBITORY FACTOR) (ASIF).
 OS BPS TAURUS (BOVINE).
 GN NPPB.

OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA;
 OC ARTIODACTYLA; RUMINANTIA; PECORA; BOVIDAE; BOVINAE; BOS.
 RN [1]
 RP SEQUENCE.
 RX MEDLINE: 90114187.
 RA NGUYEN T.T., LAZURE C., BABINSKI K., CHRETIEN M., DE LEAN A., ONG H.;
 RT "Purification and primary structure of pro-aldosterone secretion
 inhibitory factor from bovine adrenal chromaffin cells."
 RL MOL. ENDOCRINOL. 3:1823-1829(1989).
 RN [2]
 RP SEQUENCE OF 69-103.
 RX MEDLINE: 89136947.
 RA NGUYEN T.T., LAZURE C., BABINSKI K., CHRETIEN M., ONG H., DE LEAN A.;
 RT "Aldosterone secretion inhibitory factor: a novel neuropeptide in
 bovine chromaffin cells."
 RL ENDOCRINOLOGY 124:1591-1593(1989).
 CC -!- FUNCTION: INHIBITS ALDOSTERONE SECRETION.
 CC -!- FUNCTION: VASOACTIVE ACTIVITY.
 CC -!- TISSUE SPECIFICITY: BRAIN AND ALSO IN ATRIA, BUT AT MUCH LOWER
 LEVELS THAN ANP.
 CC -!- SIMILARITY: BELONGS TO THE NATRIURETIC PEPTIDES FAMILY.
 DR PIR: A41403; A41403.
 DR PROSITE: PS00263; NATRIURETIC_PEPTIDE; 1.
 DR PFAM: PF00212; ANP; 1.
 KW VASOACTIVE; BRAIN.
 FT CHAIN 1 103
 FT PEPTIDE 69 103
 FT PEPTIDE 78 103
 FT DISULFID 81 97
 SQ SEQUENCE 103 AA; 11249 MW; E3823460 CRC32;
 Query Match 77.4%; Score 106; DB 1; Length 103;
 Best Local Similarity 76.5%; Pred. No. 4.45e-12;
 Matches 13; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
 Db 81 CFCGRMDRIGVSLGCG 97
 QY 1 CFCGRMDRIGVSLGCG 17
 RESULT 15
 ID ANFC_TRISC STANDARD; PRT; 115 AA.
 AC P55208;
 DT 01-OCT-1996 (REL. 34, CREATED)
 DT 01-OCT-1996 (REL. 34, LAST SEQUENCE UPDATE)
 DT 01-OCT-1996 (REL. 34, LAST ANNOTATION UPDATE)
 DE C-TYPE NATRIURETIC PEPTIDE (CNP-115).
 OS TRIAKIS SCYLLIUM (LEOPARD SHARK) (TRIAKIS SCYLLIA).
 OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; CHONDRICHTHYES;
 OC ELASMOBRANCHII; CARCHARINIFORMES; TRIAKIDAE; TRIAKIS.
 RN [1]
 RP SEQUENCE.
 RC TISSUE-HEART, AND BRAIN;
 RX MEDLINE: 93115619.
 RA SUZUKI R., TAKAHASHI A., TAKEI Y.;
 RT "Different molecular forms of C-type natriuretic peptide isolated
 from the brain and heart of an elasmobranch, Triakis scyllia."
 RL J. ENDOCRINOL. 135:317-323(1992).
 CC -!- FUNCTION: VASORELAXANT ACTIVITY. HAS A CGMP-STIMULATING ACTIVITY
 (BY SIMILARITY).
 CC -!- TISSUE SPECIFICITY: CNP-115 IS DIFFERENTIALLY PROCESSED TO
 PRODUCE CNP-38 AND CNP-39 IN THE HEART AND CNP-22 IN THE BRAIN.
 CC -!- SIMILARITY: BELONGS TO THE NATRIURETIC PEPTIDES FAMILY.
 DR PROSITE: PS00263; NATRIURETIC_PEPTIDE; 1.
 DR PFAM: PF00212; ANP; 1.
 KW VASOACTIVE.
 FT PEPTIDE 77 115
 FT PEPTIDE 78 115
 FT PEPTIDE 94 115
 FT DISULFID 99 115
 SQ SEQUENCE 115 AA; 12904 MW; 7488BCC0 CRC32;
 Query Match 77.4%; Score 106; DB 1; Length 115;

Best Local Similarity 76.5%; Pred. No. 4.45e-12;
Matches 13; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Db 99 CFGVKLDRIQAMSLGC 115
|||.:| ||||| |||||
Oy 1 CFGGRMDRIQAMSLGC 17

Search completed: Wed Jun 16 13:15:17 1999
Job time : 7 secs.

[W][A][T][E][R][M][A][N]
[P][R][O][T][E][I][N]
[S][E][Q][U][E][N][C][E]
[I][D]: [US0902777B-1] (TM)

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MPSrch_pp protein - protein database search, using Smith-Waterman algorithm
Run on: Wed Jun 16 13:15:34 1999; MasPar time 4.67 Seconds
Tabular output not generated. 198.730 Million cell updates/sec

Title: >US-09-027-777B-1
Description: (1-17) from US0902777B.pep
Perfect Score: 137
Sequence: 1 CFGGRMDRIGAQSGLGC 17

Scoring table: PAM 150
Gap 15

Searched: 179066 seqs, 54579741 residues

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database: sptrembl9
1:sp-archaea 2:sp-bacteria 3:sp-fungi 4:sp-human
5:sp-invertebrate 6:sp-mammal 7:sp-mhc 8:sp-organelle
9:sp-phage 10:sp-plant 11:sp-rodent 12:sp-unclassified
13:sp-vertebrate 14:sp-virus

Statistics: Mean 26.929; Variance 35.212; scale 0.765

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description	Pred. No.
1	137	100.0	151	4 Q13766	ATRIAL NATRIURETIC FAC	3.71e-19
2	137	100.0	152	6 Q46540	ATRIAL NATRIURETIC PEP	3.71e-19
3	137	100.0	155	6 Q29130	CARDIODILATIN, ATRIAL	3.71e-19
4	106	77.4	129	6 Q46541	BRAIN NATRIURETIC PEP	5.15e-11
5	86	62.8	121	11 Q5086	BRAIN NATRIURETIC PEP	4.04e-06
6	86	62.8	139	13 P79799	NATRIURETIC PEPTIDE.	4.04e-06
7	62	45.3	336	4 Q92623	MYELOBLAST KIAA0227 (F	7.33e-01
8	60	43.8	454	2 Q67373	UDP-N-ACETYLURAMATE-A	1.82e+00
9	60	43.8	539	4 Q15860	VAV ONCOGENE (FRAGMENT	1.82e+00
10	59	43.1	281	5 Q19208	COSMID F08F8.	2.84e+00
11	59	43.1	307	2 Q52960	UNKNOWN PRODUCT.	2.84e+00
12	59	43.1	332	5 Q19209	COSMID F08F8.	2.84e+00
13	59	43.1	394	2 P72780	PROTEASE HH0A.	2.84e+00
14	59	43.1	634	11 Q61510	ESTROGEN-RESPONSIVE FI	2.84e+00
15	59	43.1	802	2 Q68595	HYDROXAMATE-TYPE FERRI	2.84e+00
16	58	42.3	158	10 Q49355	DIHYDRODIPICOLINATE SY	4.42e+00
17	58	42.3	289	2 Q51585	HYPOTHETICAL 32.3 KD P	4.42e+00
18	58	42.3	356	2 Q87498	ALANINE RACEMASE (EC 5	4.42e+00
19	57	41.6	402	2 P77902	PROBABLE CYTOCHROME P4	6.84e+00
20	57	41.6	404	2 Q54302	CYTOCHROME P450.	6.84e+00

21	57	41.6	416	1 O54549	ORF H1777.	6.84e+00
22	57	41.6	432	2 O25371	HYPOTHETICAL 48.8 KD P	6.84e+00
23	57	41.6	496	2 O24896	PROLINE PERMEASE (PUTP	6.84e+00
24	57	41.6	630	4 Q14258	ESTROGEN RESPONSIVE FI	6.84e+00
25	57	41.6	875	3 O42804	TRANSCRIPTIONAL ACTIVA	6.84e+00
26	56	40.9	134	2 O53503	HYPOTHETICAL 14.6 KD P	1.05e+01
27	56	40.9	295	5 Q19744	SIMILAR TO MOUSE CREB-	1.05e+01
28	56	40.9	604	5 O62315	M01G12.12 PROTEIN (FRA	1.05e+01
29	56	40.9	702	10 O82475	ARGININE DECARBOXYLASE	1.05e+01
30	56	40.9	763	5 O45732	T02E9.3 PROTEIN.	1.05e+01
31	56	40.9	824	2 O66728	POLY A POLYMERASE.	1.05e+01
32	56	40.9	866	4 O43844	IL-17 RECEPTOR.	1.05e+01
33	56	40.9	1043	5 O01757	SIMILAR TO ACHLYA AMBI	1.05e+01
34	56	40.9	1228	2 Q44334	PROLINE DEHYDROGENASE.	1.05e+01
35	56	40.9	1566	4 Q43810	RB18A PROTEIN.	1.05e+01
36	55	40.1	373	10 O24017	RESISTANCE COMPLEX PRO	1.61e+01
37	55	40.1	479	1 O26407	CONSERVED PROTEIN	1.61e+01
38	55	40.1	970	10 O80790	REVERSE-TRANSCRIPTASE-	1.61e+01
39	55	40.1	1163	5 Q26654	STORAGE PROTEIN-BINDIN	1.61e+01
40	54	39.4	179	2 O32697	METHANOL DEHYDROGENASE	2.45e+01
41	54	39.4	190	5 P91585	COS41.7.	2.45e+01
42	54	39.4	248	1 O27590	NITRATE ASSIMILATION P	2.45e+01
43	54	39.4	286	13 Q98948	SINGLE-STRAND DNA-BIND	2.45e+01
44	54	39.4	405	2 O53380	PENICILLIN-BINDING PRO	2.45e+01
45	54	39.4	1081	10 O65338	CELLULOSE SYNTHASE (FR	2.45e+01

ALIGNMENTS

RESULT	1						
ID	Q13766	FREELIMINARY;	PRT;	151	AA.		
AC	Q13766;						
DT	01-NOV-1996	(TREMBREL. 01, CREATED)					
DT	01-NOV-1996	(TREMBREL. 01, LAST SEQUENCE UPDATE)					
DT	01-JAN-1999	(TREMBREL. 09, LAST ANNOTATION UPDATE)					
DE	ATRIAL NATRIURETIC FACTOR PRECURSOR.						
OS	HOMO SAPIENS (HUMAN).						
OC	EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA; PRIMATES;						
CC	CATARRHINI; HOMINIDAE; HOMO.						
RN	[1]						
RP	SEQUENCE FROM N.A.						
RX	MEDLINE: 85206210.						
RA	SEIDMAN C.E., BLOCH K.D., ZISFEIN J., SMIT J., HABER E., HOMCY C.,						
RA	DUBY A.D., CHOI E., GRAHAM R.M., SEIDMAN J.G.						
RT	"Molecular studies of the atrial natriuretic factor gene."						
RL	HYPERTENSION 7:31-34(1985).						
DR	EMBL; M54947; G178638;						
DR	EMBL; M54951; G178638; JOINED.						
DR	PROSITE; PS00263; NATRIURETIC_PEPTIDE; 1.						
DR	PFAM; PF00212; ANP; 1.						
KW	VASOACTIVE; SIGNAL.						
FT	SIGNAL	1	25				
FT	PEPTIDE	26	55				
FT	PEPTIDE	124	151				
FT	DISULFID	130	146				
SQ	SEQUENCE	151	AA; 16381	MM; E8827DA3	CRC32;		
Query Match	100.0%;	Score	137;	DB	4;	Length	151;
Best Local Similarity	100.0%;	Pred. No.	3.71e-19;				
Matches	17;	Conservative	0;	Mismatches	0;	Indels	0;
Gaps	0;						
Db	130	CFGGRMDRIGAQSGLGC	146				
QY	1	CFGGRMDRIGAQSGLGC	17				
RESULT	2						
ID	Q46540	FREELIMINARY;	PRT;	152	AA.		
AC	Q46540;						
DT	01-JUN-1998	(TREMBREL. 06, CREATED)					
DT	01-JUN-1998	(TREMBREL. 06, LAST SEQUENCE UPDATE)					
DT	01-AUG-1998	(TREMBREL. 07, LAST ANNOTATION UPDATE)					
DE	ATRIAL NATRIURETIC PEPTIDE.						

GN ANP.
OS OVIS ARIES (SHEEP).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA;
OC ARTIODACTYLA; RUMINANTIA; PECORA; BOVOIDEA; BOVIDAE; CAPRINAE; OVIS.
RN [1]
RP SEQUENCE FROM N.A.
RA AITKEN G.D., RAIZIS A.M., GEORGE P.M., ESPINER E.A., CAMERON V.A.;
RL SUBMITTED (DEC-1997) TO EMBL/GENBANK/DBJ DATA BANKS.
DR EMBL: AF037465; G2708650;
DR PROSITE: PS00263; NATRIURETIC_PEPTIDE; 1.
SQ SEQUENCE 152 AA; 16368 MW; D53608CC CRC32;

Query Match 100.0%; Score 137; DB 6; Length 152;
Best Local Similarity 100.0%; Pred. No. 3.71e-19;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 129 CFGGRMDRIGASGLGC 145
QY 1 CFGGRMDRIGASGLGC 17
|||||

RESULT 3 PRELIMINARY; PRT; 155 AA.
ID Q29130
AC Q29130;
DT 01-NOV-1996 (TREMBLREL. 01, CREATED)
DT 01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)
DT 01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)
DE CARDIOLILIN, ATRIAL NATRIURETIC PEPTIDE.
OS TUPAIA BELANGERI.
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA;
OC SCANDENTIA; TUPAIIDAE; TUPAIA.
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=HEART;
RX SCHNEIDEMANN S., MAEGERT H.J., FORSMANN W.G.;
RA SUBMITTED (MAR-1996) TO EMBL/GENBANK/DBJ DATA BANKS.
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=HEART;
RA PARDIGOL A.;
RL SUBMITTED (MAR-1996) TO EMBL/GENBANK/DBJ DATA BANKS.
DR EMBL: Z70294; E233859;
DR PROSITE: PS00263; NATRIURETIC_PEPTIDE; 1.
DR PFAM: PF00212; ANP; 1.
SQ SEQUENCE 155 AA; 16860 MW; 77E8CA8B CRC32;

Query Match 100.0%; Score 137; DB 6; Length 155;
Best Local Similarity 100.0%; Pred. No. 3.71e-19;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 132 CFGGRMDRIGASGLGC 148
QY 1 CFGGRMDRIGASGLGC 17
|||||

RESULT 4 PRELIMINARY; PRT; 129 AA.
ID Q46541
AC Q46541;
DT 01-JUN-1998 (TREMBLREL. 06, CREATED)
DT 01-JUN-1998 (TREMBLREL. 06, LAST SEQUENCE UPDATE)
DT 01-AUG-1998 (TREMBLREL. 07, LAST ANNOTATION UPDATE)
DE BRAIN NATRIURETIC PEPTIDE.
GN BNP.
OS OVIS ARIES (SHEEP).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA;
OC ARTIODACTYLA; RUMINANTIA; PECORA; BOVOIDEA; BOVIDAE; CAPRINAE; OVIS.
RN [1]
RP SEQUENCE FROM N.A.
RA AITKEN G.D., RAIZIS A.M., GEORGE P.M., ESPINER E.A., CAMERON V.A.;
RL SUBMITTED (DEC-1997) TO EMBL/GENBANK/DBJ DATA BANKS.
DR EMBL: AF037466; G2708652;
DR PROSITE: PS00263; NATRIURETIC_PEPTIDE; 1.
SQ SEQUENCE 129 AA; 14118 MW; 85DE4222 CRC32;

Query Match 77.4%; Score 106; DB 6; Length 129;
Best Local Similarity 76.5%; Pred. No. 5.15e-11;
Matches 13; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Db 107 CFGRRLDRIQSGSLGC 123
QY 1 CFGRRMDRIGASGLGC 17
|||||

RESULT 5 PRELIMINARY; PRT; 121 AA.
ID O55086
AC O55086;
DT 01-JUN-1998 (TREMBLREL. 06, CREATED)
DT 01-JUN-1998 (TREMBLREL. 06, LAST SEQUENCE UPDATE)
DT 01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)
DE BRAIN NATRIURETIC PEPTIDE.
GN BNP.
OS MUS MUSCULUS (MOUSE).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA; RODENTIA;
OC SCIUROGNATHI; MURIDAE; MURINAE; MUS.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=129/SV;
RX MEDLINE: 94237953.
RA OGAWA Y., ITOH H., TAMURA N., SUGA S., YOSHIMASA T., UEHIRA M.,
RA MATSUDA S., SHIONO S., NISHIMOTO H., NAKAO K.;
RT "Molecular cloning of the complementary DNA and gene that encode mouse brain natriuretic peptide and generation of transgenic mice that overexpress the brain natriuretic peptide gene."
RL J. CLIN. INVEST. 93:1911-1921(1994).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=129/SV;
RX MEDLINE: 97031884.
RA TAMURA N., OGAWA Y., YASODA A., NAKAO K.;
RT "Two cardiac natriuretic peptide genes (atrial natriuretic peptide and brain natriuretic peptide) are organized in tandem in the mouse and human genomes."
RL J. MOL. CELL. CARDIOL. 28:1811-1815(1996).
DR EMBL: D82049; D1025069;
DR PROSITE: PS00263; NATRIURETIC_PEPTIDE; 1.
SQ SEQUENCE 121 AA; 13730 MW; E3BFEC0B CRC32;

Query Match 62.8%; Score 86; DB 11; Length 121;
Best Local Similarity 64.7%; Pred. No. 4.04e-06;
Matches 11; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

Db 99 CFGHKIDRIGSVSLGC 115
QY 1 CFGRRMDRIGASGLGC 17
|||||

RESULT 6 PRELIMINARY; PRT; 139 AA.
ID P79799
AC P79799;
DT 01-MAY-1997 (TREMBLREL. 03, CREATED)
DT 01-MAY-1997 (TREMBLREL. 03, LAST SEQUENCE UPDATE)
DT 01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)
DE NATRIURETIC PEPTIDE.
OS MICRURUS CORALLINUS.
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; LEPIDOSAURIA; SQUAMATA;
OC SCLEROGLOSSA; SERPENTES; COLUBROIDEA; ELAPIDAE; MICRURUS.
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=VENOM GLAND;
RA HO P.L., SOARES M.B., YAMANE T., RAW I.;
RL J. TOXICOL. TOXIN. REV. 14:327-337(1995).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=VENOM GLAND;
RX MEDLINE: 98092299.
RA HO P.L., SOARES M.B., MAACK T., GIMENEZ I., PUERTO G., FUERTADO M.F.D.,

RA RAW I.;
 RT "Cloning of an unusual natriuretic peptide from the South American
 coral snake *Micrurus corallinus*.";
 RL EUR. J. BIOCHEM. 250:144-149(1997).
 DR EMBL: U77596; G1684874;
 DR PROSITE: PS00263; NATRIURETIC_PEPTIDE; 1;
 DR PFAM: PF00112; ANP; 1.
 SQ SEQUENCE 139 AA; 14881 MW; 05421ABB CRC32;
 Query Match 62.8%; Score 86; DB 13; Length 139;
 Best Local Similarity 64.7%; Pred. No. 4.04e-06;
 Matches 11; Conservative 2; Mismatches 4; Indels 0; Gaps 0;
 Db 86 CFCQRIDRICNVSGMGC 102
 ||||| 1:111 11:11
 QY 1 CFCGRMDRIGAQSGLG 17
 RESULT 7
 ID Q92623 PRELIMINARY; PRT; 336 AA.
 AC Q92623;
 DT 01-FEB-1997 (TREMBLREL. 02, CREATED)
 DT 01-FEB-1997 (TREMBLREL. 02, LAST SEQUENCE UPDATE)
 DT 01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)
 DE MIELOBLAST KIAA0227 (FRAGMENT).
 GN KIAA0227.
 OS HOMO SAPIENS (HUMAN).
 OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA; PRIMATES;
 OC CATARRHINI; HOMINIDAE; HOMO.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE-BONE MARROW;
 RX MEDLINE; 97191544.
 RA NAGASE T., SEKI N., ISHIKAWA K., OHIRA M., KAWARABAYASI Y., OHARA O.,
 RA TANAKA A., KOTANI H., MIYAJIMA N., NOMURA N.;
 RT "Prediction of the coding sequences of unidentified human genes. VI.
 RT The coding sequences of 80 new genes (K1AA0201-K1AA0280) deduced by
 RT analysis of cDNA clones from cell line KG-1 and brain.";
 RL DNA RES. 3:321-329(1996).
 DR EMBL: D86980; D1013905;
 DR PFAM: PF00515; TPR; 1.
 FT NON_TER 1
 SQ SEQUENCE 336 AA; 35417 MW; 62C3199B CRC32;
 Query Match 45.3%; Score 62; DB 4; Length 336;
 Best Local Similarity 58.3%; Pred. No. 7.33e-01;
 Matches 7; Conservative 3; Mismatches 2; Indels 0; Gaps 0;
 Db 112 GGRMERKGSAG 123
 ||||| 1:1
 QY 3 GGRMDRIGAQSGLG 14
 RESULT 8
 ID O67373 PRELIMINARY; PRT; 454 AA.
 AC O67373;
 DT 01-AUG-1998 (TREMBLREL. 07, CREATED)
 DT 01-AUG-1998 (TREMBLREL. 07, LAST SEQUENCE UPDATE)
 DT 01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)
 DE UDP-N-ACETYLURAMATE-ALANINE LIGASE.
 GN MURC.
 OS AQUIFEX AEOLICUS.
 OC BACTERIA; AQUIFICALES; AQUIFICACEAE; AQUIFEX.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-VF5;
 RX MEDLINE; 98196666.
 RA DECKERT G., WARREN P.V., GAASTERLAND T., YOUNG W.G., LENOX A.L.,
 RA GRAHAM D.E., OVERBECK R., SNEAD M.A., KELLER M., AUJAY M., HUBER R.,
 RA FELDMAN R.A., SHORT J.M., OLSON G.J., SWANSON R.V.;
 RT "The complete genome of the hyperthermophilic bacterium *Aquifex
 aeolicus*.";
 RL NATURE 392:353-358(1998).

RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN-VF5;
 RA DECKERT G., WARREN P.V., GAASTERLAND T., YOUNG W.G., LENOX A.L.,
 RA GRAHAM D.E., OVERBECK R., SNEAD M.A., KELLER M., AUJAY M., HUBER R.,
 RA FELDMAN R.A., SHORT J.M., OLSON G.J., SWANSON R.V.;
 RL SUBMITTED (JUL-1997) TO EMBL/GENBANK/DBJ DATA BANKS.
 DR EMBL: AE000736; G2983764;
 KW LIGASE.
 SQ SEQUENCE 454 AA; 50893 MW; 1207F9CE CRC32;
 Query Match 43.8%; Score 60; DB 2; Length 454;
 Best Local Similarity 46.7%; Pred. No. 1.82e+00;
 Matches 7; Conservative 5; Mismatches 3; Indels 0; Gaps 0;
 Db 139 IGGRLKRLGNAKLG 153
 :|||: 1:1: 11
 QY 2 FCGRMDRIGAQSGLG 16
 RESULT 9
 ID Q15860 PRELIMINARY; PRT; 539 AA.
 AC Q15860;
 DT 01-NOV-1996 (TREMBLREL. 01, CREATED)
 DT 01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)
 DT 01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)
 DE VAV ONCOGENE (FRAGMENT).
 GN VAV.
 OS HOMO SAPIENS (HUMAN).
 OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA; PRIMATES;
 OC CATARRHINI; HOMINIDAE; HOMO.
 RN [1]
 RP SEQUENCE FROM N.A.
 RA ROMERO F.;
 RL SUBMITTED (JAN-1995) TO EMBL/GENBANK/DBJ DATA BANKS.
 RN [2]
 RP SEQUENCE OF 1-36 FROM N.A.
 RA RAMOS-MORALES F., ROMERO F., SCHWEIGHOFFER F., BISMUTH G., CAMONIS J.,
 RA TORTOLERO M., FISCHER S.;
 RL ONCOGENE 11:1665-1669(1995).
 RN [3]
 RP SEQUENCE FROM N.A.
 RA ROMERO F.;
 RL SUBMITTED (MAR-1995) TO EMBL/GENBANK/DBJ DATA BANKS.
 DR EMBL: X83931; E135630;
 DR PROSITE: PS00479; DAG_PE_BINDING_DOMAIN; 1.
 DR PROSITE: PS00741; GDS_CDC24; 1.
 DR PFAM: PF00017; SH2; 1.
 DR PFAM: PF00018; SH3; 2.
 DR PFAM: PF00130; DAG_PE-bind; 1.
 DR PFAM: PF00169; PH; 1.
 KW PHORBOL-ESTER BINDING.
 FT NON_TER 1
 FT NON_TER 539 539
 SQ SEQUENCE 539 AA; 62607 MW; AF558B9B CRC32;
 Query Match 43.8%; Score 60; DB 4; Length 539;
 Best Local Similarity 46.7%; Pred. No. 1.82e+00;
 Matches 7; Conservative 5; Mismatches 3; Indels 0; Gaps 0;
 Db 374 YAGPMERAGAESILA 388
 :|| 1:1 11:11
 QY 2 FCGRMDRIGAQSGLG 16
 RESULT 10
 ID Q19208 PRELIMINARY; PRT; 281 AA.
 AC Q19208;
 DT 01-NOV-1996 (TREMBLREL. 01, CREATED)
 DT 01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)
 DT 01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)
 DE COSMID F08F8.
 GN F08F8.5.

OS CAENORHABDITIS ELEGANS.
 OC EUKARYOTA; METAZOA; NEMATODA; SECERNENTEA; RHABDITIA; RHABDITIDA;
 OC RHABDITINA; RHABDITOIDEA; RHABDITIDAE; PELODERINAE; CAENORHABDITIS.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-BRISTOL N2;
 RX MEDLINE; 94150718.
 RA WILSON R., AINSOUGH R., ANDERSON K., BAYNES C., BERKS M.,
 RA BONFIELD J., BURTON J., CONNELL M., COPSEY T., COOPER J., COULSON A.,
 RA CRAXTON M., DEAR S., DU Z., DURBIN R., FAVELLO A., FULTON L.,
 RA GARDNER A., GREEN P., HAWKINS T., HILLIER L., JIER M., JOHNSTON L.,
 RA JONES M., KERSHAW J., KIRSTEN J., LAISTER N., LATREILLE P.,
 RA LIGHTNING J., LLOYD C., MCMURRAY A., MORTIMORE B., O'CALLAGHAN M.,
 RA PARSONS J., PERCY C., RIFKEN L., ROOPRA A., SAUNDERS D., SHOWNKEEN R.,
 RA SMALDON N., SMITH A., SONNHAMMER E., STADEN R., SULSTON J.,
 RA THIERRY-MIEG J., THOMAS K., VAUDIN M., VAUGHAN K., WATERSTON R.,
 RA WATSON A., WEINSTOCK L., WILKINSON-SPROAT J., WOHLDMAN P.;
 RT *2.2 Mb of contiguous nucleotide sequence from chromosome III of C.
 RT elegans.;
 RL NATURE 368:32-38(1994).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN-BRISTOL N2;
 RX WATERSTON R.;
 RA SUBMITTED (JUN-1995) TO EMBL/GENBANK/DBJ DATA BANKS.
 RL EMBL; U28991; G861368; -;
 SQ SEQUENCE 281 AA; 32314 MW; A80C66BA CRC32;

Query Match 43.1%; Score 59; DB 5; Length 281;
 Best Local Similarity 50.0%; Pred. No. 2.84e+00;
 Matches 7; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

Db 176 CFGRRARSASPIG 189
 QY 1 CFGRRDRIGAQSG 14

RESULT 11
 ID Q52960 PRELIMINARY; PRT; 307 AA.
 AC Q52960;
 DT 01-NOV-1996 (TREMREL. 01, CREATED)
 DT 01-NOV-1996 (TREMREL. 01, LAST SEQUENCE UPDATE)
 DT 01-NOV-1998 (TREMREL. 08, LAST ANNOTATION UPDATE)
 DE UNKNOWN PRODUCT.
 OS RHIZOBIUM MELILOTI.
 OC BACTERIA; PROTEOBACTERIA; ALPHA SUBDIVISION; RHIZOBIACEAE GROUP;
 OC RHIZOBIACEAE; SINORHIZOBIUM.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-GR4;
 RX MEDLINE; 97074647.
 RA ZEKRI S., TORO N.;
 RT "Identification and nucleotide sequence of Rhizobium meliloti
 RT insertion sequence ISRm6, a small transposable element that belongs
 RT to the IS3 family.";
 RL GENE 175:43-48(1996).
 DR EMBL; X95567; E221839; -;
 SQ SEQUENCE 307 AA; 33688 MW; 8B9F5785 CRC32;

Query Match 43.1%; Score 59; DB 2; Length 307;
 Best Local Similarity 41.2%; Pred. No. 2.84e+00;
 Matches 7; Conservative 5; Mismatches 5; Indels 0; Gaps 0;

Db 70 CSGRRSPASTASIGC 86
 QY 1 CFGRRDRIGAQSGLCG 17

RESULT 12
 ID Q19209 PRELIMINARY; PRT; 352 AA.
 AC Q19209;
 DT 01-NOV-1996 (TREMREL. 01, CREATED)
 DT 01-NOV-1996 (TREMREL. 01, LAST SEQUENCE UPDATE)
 DT 01-NOV-1998 (TREMREL. 08, LAST ANNOTATION UPDATE)
 DE COSMD F08F8.
 GN F08F8.1.
 OS CAENORHABDITIS ELEGANS.
 OC EUKARYOTA; METAZOA; NEMATODA; SECERNENTEA; RHABDITIA; RHABDITIDA;
 OC RHABDITINA; RHABDITOIDEA; RHABDITIDAE; PELODERINAE; CAENORHABDITIS.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-BRISTOL N2;
 RX MEDLINE; 94150718.
 RA WILSON R., AINSOUGH R., ANDERSON K., BAYNES C., BERKS M.,
 RA BONFIELD J., BURTON J., CONNELL M., COPSEY T., COOPER J., COULSON A.,
 RA CRAXTON M., DEAR S., DU Z., DURBIN R., FAVELLO A., FULTON L.,
 RA GARDNER A., GREEN P., HAWKINS T., HILLIER L., JIER M., JOHNSTON L.,
 RA JONES M., KERSHAW J., KIRSTEN J., LAISTER N., LATREILLE P.,
 RA LIGHTNING J., LLOYD C., MCMURRAY A., MORTIMORE B., O'CALLAGHAN M.,
 RA PARSONS J., PERCY C., RIFKEN L., ROOPRA A., SAUNDERS D., SHOWNKEEN R.,
 RA SMALDON N., SMITH A., SONNHAMMER E., STADEN R., SULSTON J.,
 RA THIERRY-MIEG J., THOMAS K., VAUDIN M., VAUGHAN K., WATERSTON R.,
 RA WATSON A., WEINSTOCK L., WILKINSON-SPROAT J., WOHLDMAN P.;
 RT *2.2 Mb of contiguous nucleotide sequence from chromosome III of C.
 RT elegans.;
 RL NATURE 368:32-38(1994).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN-BRISTOL N2;
 RX DU Z.;
 RA SUBMITTED (JUN-1995) TO EMBL/GENBANK/DBJ DATA BANKS.
 RL EMBL; U28991; G861369; -;
 SQ SEQUENCE 352 AA; 40771 MW; 31044A7A CRC32;

Query Match 43.1%; Score 59; DB 5; Length 352;
 Best Local Similarity 50.0%; Pred. No. 2.84e+00;
 Matches 7; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

Db 102 CFGRRARSASPIG 115
 QY 1 CFGRRDRIGAQSG 14

RESULT 13
 ID P72780 PRELIMINARY; PRT; 394 AA.
 AC P72780;
 DT 01-FEB-1997 (TREMREL. 02, CREATED)
 DT 01-FEB-1997 (TREMREL. 02, LAST SEQUENCE UPDATE)
 DT 01-JAN-1999 (TREMREL. 09, LAST ANNOTATION UPDATE)
 DE PROTEASE HHOA.
 GN HHOA.
 OS SYNECHOCYSTIS SP. (STRAIN PCC 6803).
 OC BACTERIA; CYANOBACTERIA; CHROCOCCALES; SYNECHOCYSTIS.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-PCC6803;
 RA TABATA S.;
 RL SUBMITTED (JUN-1996) TO EMBL/GENBANK/DBJ DATA BANKS.
 RN [2]
 RP SEQUENCE FROM N.A.
 RX STRAIN-PCC6803;
 RX MEDLINE; 97061201.
 RA KANEKO T., SATO S., KOTANI H., TANAKA A., ASAMIZU E., NAKAMURA Y.,
 RA MIYAJIMA N., HIROSAWA M., SUGIURA M., SASAMOTO S., KIMURA T.,
 RA HOSOUCHI T., MATSUNO A., MURAKI A., NAKAZAKI N., NARUO K., OKUMURA S.,
 RA SHIMPO S., TAKEUCHI C., WADA T., WATANABE A., YAMADA M., YASUDA M.,

```

aeruginosa: cycle selection of iron-regulated genes.";
PROC. NATL. ACAD. SCI. U.S.A. 93:4409-4414 (1996).
[2]
RN      SEQUENCE FROM N.A.
RC      STRAIN-PAOI:
RA      OCHSNER U.A., VASIL A.I., JOHNSON Z., VASIL M.L.;
RL      SUBMITTED (MAR-1998) TO EMBL/GENBANK/DBJ DATA BANKS.
DR      EMBL: AF051691; G2981048; --
SQ      SEQUENCE  802 AA;  88271 MW;  02BD9E37 CRC32;

Query Match      43.1%   Score 59;  DB 2;  Length 802;
Best Local Similarity 50.0%;  Pred. No. 2.84e+00;
Matches      7;  Conservative      6;  Mismatches  1;  Indels

Db      44  LACTLNRIAAQGL 57
              : : : : : : : : : :
Qy      2  FGGRMDRIGAQSL 15

Search completed: Wed Jun 16 13:16:30 1999
Job time : 56 secs.

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AC P82556;
 DT 16-NOV-1990 (first entry)
 DE Vasodilatory peptide.
 KW vasodilatory peptide; cardionatrin.
 OS synthetic.
 PN J63107997-A.
 PD 12-MAY-1986: 220835.
 PF 18-SEP-1986: JP-220835.
 PR 18-SEP-1986: JP-220835.
 PA (MITU) Mitsubishi Chem Ind KK.
 DR WPI: 88-170991/25.
 PT Biologically prepared peptide -
 PT has vein relaxation activity.
 PS Claim 1: page 1: l3pp: Japanese
 CC This sequence was isolated from a cDNA library prepared from
 CC poly(A) mRNA isolated from human heart. Sequences complementary
 CC to the DNA encoding MDRIG of cardionatrin were isolated using
 CC a mixture of oligonucleotide probes. Two plasmids, pHAVD and pMANF,
 CC identified by this screening process, were then used to transform
 CC E.coli which were cultured to produce the peptide.
 SQ Sequence 125 AA;

Query Match 100.0%; Score 101; DB 1; Length 125;
 Best Local Similarity 100.0%; Pred. No. 1.82e-02;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 90 lralltaprsllrsls 104
 |||||
 QY 1 LRALLTAPRSLLRSS 15

RESULT 3
 ID P50037 standard; Protein: 126 AA.
 AC P50037;
 DT 03-SEP-1991 (first entry)
 DE Sequence of human gamma-atrium natriuretic polypeptide (ANP).
 KW Natriuretic; diuretic; hypotensive; antihypertensive.
 OS Homo sapiens.
 PN EP-164273-A.
 PD 11-DEC-1985.
 PF 08-JUN-1984; 116605.
 PR 08-JUN-1984: JP-116605.
 PR 08-JUN-1984: JP-116605.
 PA (SUNR) SUNTORY LTD.
 PI Matsuo H, Kangawa K, Hayashi Y, Oikawa S, Oshima T,
 PI Tanaka S, Nakazato H, Tawaragi Y;
 DR WPI: 85-312162/50.
 DR N-PSDB: N50055.
 PT New DNA sequences from human atrium cordis - coding for new
 PT diuretic polypeptide or precursor cpds.
 PS Claim 26; Page 37: 53pp; English.
 CC The precursor of human gamma-ANP and its 26Asn-151Iyr fragmentare
 CC claimed (P50036, P50037), as are the DNA SQs encoding them (N50020,
 CC N50055). The 26Asn-151Iyr fragment has a diuretic action so is
 CC useful as a hypotensive/antihypertensive agent. The usual dose is 0.
 CC 01-1 mg/kg.
 SQ Sequence 126 AA;

Query Match 100.0%; Score 101; DB 3; Length 126;
 Best Local Similarity 100.0%; Pred. No. 1.82e-02;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 90 lralltaprsllrsls 104
 |||||
 QY 1 LRALLTAPRSLLRSS 15

RESULT 4
 ID R00582 standard; protein: 126 AA.
 AC R00582;
 DT 05-JUN-1989 (first entry)
 DE Human gamma atrial natriuretic polypeptide (gamma-hANP).
 KW Gamma atrial natriuretic polypeptide; ANP; natriuretic;

hypertension; cirrhosis; nephrosis; heart disease.
 OS Homo sapiens.
 PN EP-350227-A.
 PD 10-JAN-1988.
 PF 30-JUN-1989; 306669.
 PR 04-JUL-1988: JP-166641.
 PA (SHIO) Shionogi Selyaku Kabushiki.
 PI Imura H, Nakao K;
 DR WPI: 90-009970/02.
 PT Monoclonal antibodies recognising gamma-atrial natriuretic -
 PT used for diagnosis of diseases eg kidney and heart disease.
 PS Disclosure: Fig 1: 10pp: English.
 CC Gamma-hANP of which the N-terminal 25 AAs are recognisys monoclonal
 CC antibodies of the invention
 SQ Sequence 126 AA;

Query Match 100.0%; Score 101; DB 2; Length 126;
 Best Local Similarity 100.0%; Pred. No. 1.82e-02;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 90 lralltaprsllrsls 104
 |||||
 QY 1 LRALLTAPRSLLRSS 15

RESULT 5
 ID W34533 standard; Protein: 126 AA.
 AC W34533;
 DT 24-MAR-1998 (first entry)
 DE Human atrial natriuretic factor prohormone.
 KW Human atrial natriuretic factor prohormone; therapy: hypertension;
 KW congestive heart failure; pulmonary oedema; toxemia of pregnancy;
 KW nephrotic syndrome; renal failure; hepatic cirrhosis; hyperkalemia;
 KW acidosis; digitalis overdose; insulin deficiency; Addison's disease;
 KW proANF; hyperaldosteronism.
 OS Homo sapiens.
 PN US5691310-A.
 PD 25-NOV-1997.
 PF 09-MAR-1995; 401246.
 PR 09-MAR-1995: US-401246.
 PR 29-SEP-1987: US-102477.
 PR 01-MAY-1990: US-517252.
 PR 14-NOV-1991: US-799211.
 PA (VESE/) VESELY D L.
 PI Vesely DL;
 DR WPI: 98-017684/02.
 PT Treatment of hypertension and related disorders - with synthetic
 PT peptide fragment of atrial natriuretic factor prohormone
 PS Disclosure: Column 4: 9pp; English.
 CC This sequence represents the human atrial natriuretic factor prohormone
 CC (proANF). Fragments of this sequence (see W34521-W34523) can be used in
 CC the method of the invention. The method is for treating hypertension,
 CC congestive heart failure, pulmonary oedema, toxemia of pregnancy,
 CC nephrotic syndrome, acute and chronic renal failure or hepatic cirrhosis
 CC with or without ascites comprises administering a synthetic peptide
 CC consisting of amino acids 1-30, 31-67 or 79-98 of proANF. The peptides
 CC proANF(1-30) and proANF(79-98) can also be used in a method for treating
 CC hyperkalemia associated with acidosis, digitalis overdose,
 CC succinylcholine, insulin deficiency, acute or chronic renal failure,
 CC Addison's disease or hyperaldosteronism. The peptides have hypertensive,
 CC diuretic, natriuretic and/or kalluretic activity.
 SQ Sequence 126 AA;

Query Match 100.0%; Score 101; DB 27; Length 126;
 Best Local Similarity 100.0%; Pred. No. 1.82e-02;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 90 lralltaprsllrsls 104
 |||||
 QY 1 LRALLTAPRSLLRSS 15

RESULT 6

ID P51240 standard; peptide; 126 AA.
AC P51240;
DT 03-AUG-1992 (first entry)
DE Sequence of pro-atrial natriuretic/vasodilator polypeptide
DE (ANVP).
KW Natriuretic; diuretic; vasodilator;
KW renin-angiotensin-aldosterone system.
OS Mammal.
FH Key Location/Qualifiers
FT modified_site 1
FT /label= H-M
FT disulfide_bond 105..121
FT modified_site 126
FT /label= Y-OH
FT
PN W08504870-A.
PD 07-NOV-1985.
PF 16-APR-1985; U00658.
PR 19-APR-1984; US-602117.
PR 01-JUN-1984; US-616488.
PR 20-JUN-1984; US-622639.
PA (BIOT-) BIOTECHNOL RES PART.
PI Johnson LK, Atlas SA, McCarthy BJ, Laragh JH, Lewicki JA;
DR WPI: 85-289654/46.
PT New atrial polypeptide cpds. - useful as natriuretics,
PT diuretics, vasodilators and modulators of the
PT renin-angiotensin-aldosterone system
PS Claim 8; Page 116; 144pp; English.
CC The inventors claim a polypeptide comprising atrial natriuretic/
CC vasodilator polypeptide (ANVP), pro-ANVP or pre-pro-ANVP, or their
CC fragments. The encoding DNA sequence is also claimed. The claimed
CC polypeptides are natriuretics, diuretics, vasodilators and
CC modulators of the renin-angiotensin-aldosterone system. Dose is
CC 0.01-100 ug/kg.
SQ Sequence 126 AA;

Query Match 100.0%; Score 101; DB 4; Length 126;
Best Local Similarity 100.0%; Pred. NO. 1.82e-02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 90 lralltapsrlrrss 104
|||||
QY 1 LRALLTAPRSLRRSS 15

RESULT 7
ID R36935 standard; Protein; 136 AA.
AC R36935;
DT 14-SEP-1993 (first entry)
DE Human pre-proANVP #2.
KW Human; pre-pro; atrial natriuretic/vasodilator peptide; ANVP; rat;
KW regulation; fluid volume; blood pressure.
OS Homo sapiens.
PN US5212286-A.
PD 18-MAY-1993.
PF 09-APR-1984; 602117.
PR 09-APR-1984; US-602117.
PR 01-JUN-1984; US-616488.
PR 08-MAY-1985; US-766030.
PR 05-JUN-1986; US-870795.
PA (SCIO-) SCIOS NOVA INC.
PI Lewicki JA, Scarborough RM;
DR WPI: 93-175525/21.
DR N-PSDB: Q41455.
PT New polypeptide cpd. - useful as natriuretic, diuretic and/or
PT vasodilator in mammals
PS Disclosure; Fig 18; 45pp; English.
CC This sequence is encoded by the human pre-pro atrial natriuretic/
CC vasodilator peptide (ANVP) cDNA. Fragments of this protein and the
CC corresponding sequence in rat (see also R36936), may be used for
CC regulation of fluid volume and blood pressure in host organisms.
CC The ANVP fragments may be produced by solid-phase techniques. See
CC also R36937-78.
SQ Sequence 136 AA;

Query Match 100.0%; Score 101; DB 7; Length 136;
Best Local Similarity 100.0%; Pred. NO. 1.82e-02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 100 lralltapsrlrrss 114
|||||
QY 1 LRALLTAPRSLRRSS 15

RESULT 8
ID R03301 standard; protein; 147 AA.
AC R03301;
DT 15-AUG-1990 (first entry)
DE Sequence of pre-human atrial natriuretic peptide.
KW Human-chAMP; diuretic; antihypertensivity; ss.
OS Homo sapiens.
PN J02025499-A.
PD 26-JAN-1990.
PF 14-JUL-1988; 173739.
PR 14-JUL-1988; JP-173739.
PA (MATS/) Matsuo T.
DR WPI: 90-071804/10.
PT Physio-active peptide derived from birds - has cysteine bridge,
PT specified AA sequence and diuretic and antihypertensive properties.
PS Disclosure; Fig 14; 16pp; Japanese.
CC This sequence has 99 amino acid residues homologous to the pre-chAMP.
CC See also Q03466-Q03468, R03301 and R03402.
SQ Sequence 147 AA;

Query Match 100.0%; Score 101; DB 1; Length 147;
Best Local Similarity 100.0%; Pred. NO. 1.82e-02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 111 lralltapsrlrrss 125
|||||
QY 1 LRALLTAPRSLRRSS 15

RESULT 9
ID P51241 standard; peptide; 150 AA.
AC P51241;
DT 03-AUG-1992 (first entry)
DE Sequence of pre-pro-atrial natriuretic/vasodilator
DE polypeptide (ANVP).
KW Natriuretic; diuretic; vasodilator;
KW renin-angiotensin-aldosterone system.
OS Homo sapiens.
FH Key Location/Qualifiers
FT misc_difference 16..41
FT /note= "encoded by N50763"
PN W08504870-A.
PD 07-NOV-1985.
PF 16-APR-1985; U00658.
PR 19-APR-1984; US-602117.
PR 01-JUN-1984; US-616488.
PR 20-JUN-1984; US-622639.
PA (BIOT-) BIOTECHNOL RES PART.
PI Johnson LK, Atlas SA, McCarthy BJ, Laragh JH, Lewicki JA;
DR WPI: 85-289654/46.
DR N-PSDB: N50695, N50763.
PT New atrial polypeptide cpds. - useful as natriuretics,
PT diuretics, vasodilators and modulators of the
PT renin-angiotensin-aldosterone system
PS Example; Fig 1A; 144pp; English.
CC The inventors claim a polypeptide comprising atrial natriuretic/
CC vasodilator polypeptide (ANVP), pro-ANVP or pre-pro-ANVP, or their
CC fragments. The encoding DNA sequence is also claimed. The claimed
CC polypeptides are natriuretics, diuretics, vasodilators and
CC modulators of the renin-angiotensin-aldosterone system. Dose is
CC 0.01-100 ug/kg.
SQ Sequence 150 AA;

Query Match 100.0%; Score 101; DB 4; Length 150;
 Best Local Similarity 100.0%; Pred. No. 1.82e-02;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DB 115 lraltapsrlrrss 129
 |||||
 QY 1 LRALLTAPRSLRRSS 15

RESULT 10
 ID P51239 standard; peptide; 150 AA.
 AC P51239;
 DT 03-AUG-1992 (first entry)
 DE Sequence of pre-pro-atrial natriuretic/vasodilator polypeptide (ANVP).
 DE Natriuretic; diuretic; vasodilator;
 KW venin-angiotensin-aldosterone-system.
 OS Mammal.
 FH Key Location/Qualifiers
 FT modified_site 1 /label= H-M
 FT disulfide_bond 130..146
 FT modified_site 151 /label= Y-OH
 FT W08504870-A.
 PN 07-NOV-1985.
 PD 16-APR-1985; U00658.
 PF 19-APR-1984; US-602117.
 PR 01-JUN-1984; US-616488.
 PR 20-JUN-1984; US-622639.
 PA (BIOT-) BIOTECHNOL RES PART.
 PI Johnson LK, Atlas SA, McCarthy BJ, Laragh JH, Lewicki JN;
 DR WPI; 85-289654/46.
 DT New atrial polypeptide cpds. - useful as natriuretics,
 PT diuretics, vasodilators and modulators of the
 PT renin-angiotensin-aldosterone system
 PS Claim 7; Page 115; 144pp; English.
 CC The inventors claim a polypeptide comprising atrial natriuretic/
 CC vasodilator polypeptide (ANVP), pro-ANVP or pre-pro-ANVP, or their
 CC fragments. The encoding DNA sequence is also claimed. The claimed
 CC polypeptides are natriuretics, diuretics, vasodilators and
 CC modulators of the renin-angiotensin-aldosterone system. Dose is
 CC 0.01-100 ug/kg.
 SQ Sequence 150 AA;

Query Match 100.0%; Score 101; DB 4; Length 150;
 Best Local Similarity 100.0%; Pred. No. 1.82e-02;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DB 115 lraltapsrlrrss 129
 |||||
 QY 1 LRALLTAPRSLRRSS 15

RESULT 11
 ID P70629 standard; protein; 151 AA.
 AC P70629;
 DT 09-APR-1991 (first entry)
 DE Sequence encoded by human atrial natriuretic peptide factor (ANF) gene.
 DE DNA fingerprinting; probe; hypertension.
 OS Homo sapiens.
 PN W08702709-A.
 PD 07-MAY-1987.
 PF 24-OCT-1986; U02293.
 PR 24-OCT-1985; US-790813.
 PR 12-NOV-1985; US-796904.
 PR 09-JAN-1986; US-817433.
 PR 11-JUN-1986; US-873199.
 PA (BIOT-) BIOTECHN RES PARTN.
 PI Shine J, Baker AR, Frossard PM;
 DR WPI; 87-136035/19.
 DR N-PSDB; N70974.

PT Genetic analysis diagnostic for hypertension - by detecting
 PT polymorphous of the renin, kallikrein or ANF gene regions
 PS Disclosure: Fig 2; 31pp; English.
 CC The patent application is for a method used for determin. of a
 CC genetic fingerprint of a subject which allows early diagnosis of
 CC individuals at risk of hypertension and permits early therapeutic
 CC measures to prevent the fatal symptomology of the disease. The
 CC section of the genome which is fingerprinted or otherwise subject to
 CC study using the results is dependent on the nature of the probe.
 CC The probes useful in the present invention are selected from the
 CC renin, kallikrein, or ANF gene (see FT).
 SQ Sequence 151 AA;

Query Match 100.0%; Score 101; DB 2; Length 151;
 Best Local Similarity 100.0%; Pred. No. 1.82e-02;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DB 115 lraltapsrlrrss 129
 |||||
 QY 1 LRALLTAPRSLRRSS 15

RESULT 12
 ID P50036 standard; Protein; 151 AA.
 AC P50036;
 DT 03-SEP-1991 (first entry)
 DE Sequence of the precursor of human gamma-atrium natriuretic
 DE polypeptide (ANP).
 KW Natriuretic; diuretic; hypotensive; antihypertensive.
 OS Homo sapiens.
 PN EP-164273-A.
 PD 11-DEC-1985.
 PF 08-JUN-1984; 116605.
 PR 08-JUN-1984; JP-116606.
 PR 08-JUN-1984; JP-116605.
 PA (SUNR) SUNTORY LTD.
 PI Matsuo H, Kangawa K, Hayashi Y, Oikawa S, Oshima T,
 PI Tanaka S, Nakazato H, Tawaragi Y;
 DR WPI; 85-312162/50.
 DR N-PSDB; N50020.
 DT New DNA sequences from human atrium cordis - coding for new
 PT diuretic polypeptide or precursor cpds.
 PS Claim 25; Fig 5; 53pp; English.
 CC The precursor of human gamma-ANP and its 26Asn-151Tyr fragmentare
 CC claimed (P50036, P50037), as are the DNA SQs encoding them (N50020,
 CC N50035). The 26Asn-151Tyr fragment has a diuretic action so is
 CC useful as a hypotensive/antihypertensive agent. The usual dose is 0.
 CC 01-1 mg/kg.
 SQ Sequence 151 AA;

Query Match 100.0%; Score 101; DB 3; Length 151;
 Best Local Similarity 100.0%; Pred. No. 1.82e-02;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DB 115 lraltapsrlrrss 129
 |||||
 QY 1 LRALLTAPRSLRRSS 15

RESULT 13
 ID P50050 standard; protein; 151 AA.
 AC P50050;
 DT 28-OCT-1991 (first entry)
 DE Cardiodilatin peptide.
 KW Cardiodilatin; plasmid pHANF48; muscle relaxant; antihypertensive.
 OS Homo sapiens.
 PN EP-159943-A.
 PD 30-OCT-1985.
 PF 11-APR-1985; 400725.
 PR 12-APR-1984; JP-073663.
 PR 21-JUN-1984; JP-128335.
 PR 16-AUG-1984; JP-170739.
 PR 12-OCT-1984; JP-213897.

PA (MITU) Mitsubishi Chemical Industries Ltd.
 PI Nakanishi S, Teranishi Y, Nagahari K, Shibui T, Takamatsu K;
 DR WPI; 85-2711495/44.
 DR N-PSDB: N50069.
 PT Expression vector contg. gene for cardionatriin or cardiodilatin - and
 PT corresp. DNA sequences, useful as antihypertensive agents.
 PS Disclosure; Fig. 13; 45pp; English.
 CC The DNA encoding the cardiodilatin is carried on plasmid PHANF48.
 CC Cardiodilatin is a muscle relaxant, so is useful as an antihypertensive
 CC agent. The DNA is obtd. from RNA isolated from the human heart.
 SQ Sequence 151 AA;

Query Match 100.0%; Score 101; DB 3; Length 151;
 Best Local Similarity 100.0%; Pred. No. 1.82e-02;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 115 lraltapsrlrrss 129
 Qy 1 LRALLTAPRSLRRSS 15

RESULT 14
 ID R36934 standard; Protein; 151 AA.

AC R36934; 1993 (first entry)
 DT 14-SEP-1993
 DE Human pre-proANVP #1.
 KW Human; pre-pro; atrial natriuretic/vasodilator peptide; ANVP; rat;
 OS regulation; fluid volume; blood pressure.

OS Homo sapiens.

FT Key Location/Qualifiers

FT peptide 1..41

FT protein /note= "Signal peptide"

FT 42..151

FT /note= "Mature protein"

PN US5212286-A.

PD 18-MAY-1993.

PF 09-APR-1984; 602117.

PR 09-APR-1984; US-602117.

PR 01-JUN-1984; US-616488.

PR 08-MAY-1985; US-766030.

PR 05-JUN-1986; US-870795.

PA (SCIO-) SCIOS NOVA INC.

PI Lewicki JA, Scarborough RM;

DR WPI; 93-175525/21.

DR N-PSDB: Q41454.

PT New polypeptide cpd. - useful as natriuretic, diuretic and/or

PT vasodilator in mammals

PS Disclosure; Fig 1A; 45pp; English.

CC This sequence is encoded by the human pre-pro atrial natriuretic/

CC vasodilator peptide (ANVP) DNA. Fragments of this protein and the

CC corresponding sequence in rat (see also R36936), may be used for

CC regulation of fluid volume and blood pressure in host organisms.

CC The ANVP fragments may be produced by solid-phase techniques. See

CC also R36937-78.

SQ Sequence 151 AA;

Query Match 100.0%; Score 101; DB 7; Length 151;
 Best Local Similarity 100.0%; Pred. No. 1.82e-02;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 115 lraltapsrlrrss 129
 Qy 1 LRALLTAPRSLRRSS 15

RESULT 15

ID P50115 standard; peptide; 48 AA.

AC P50115;

DT 22-OCT-1991 (first entry)

DE Rat atrial natriuretic factor-beta.

KW Atrial natriuretic factor; diuretic; hypotensive.

OS Rattus rattus.

FH Key Location/Qualifiers

FT disulfide_bond 27..43
 PN EP-153865-A.
 PD 04-SEP-1985.
 PF 28-FEB-1985; 301364.
 PR 02-MAR-1984; JP-038816.
 PA (SUNR) SUNTORY LTD.
 PI Matsuo H, Kangawa K;
 DR WPI; 85-218548/36.
 PT New diuretic, antihypertensive polypeptide - isolated from rat
 PT atrium cordis.

PS Claim 1; Page 17; 23pp; English.
 CC The rat atrial natriuretic factor-beta has diuretic, natriuretic and
 CC hypotensive or hypertensive activity.
 SQ Sequence 48 AA;

Query Match 94.1%; Score 95; DB 3; Length 48;
 Best Local Similarity 86.7%; Pred. No. 6.74e-02;
 Matches 13; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Db 12 lraltagprslrrss 26
 Qy 1 LRALLTAPRSLRRSS 15

Search completed: Wed Jun 16 13:18:45 1999
 Job time : 18 secs.

WATERMAN

(TM)

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MPsrch_pp protein - protein database search, using Smith-Waterman algorithm

Run On: Wed Jun 16 13:21:01 1999; MasPar time 1.40 Seconds
Tabular output not generated. 108.644 Million cell updates/sec

Title: >US-09-027-777B-2
Description: (1-15) from US0902777B.pep
Perfect Score: 101
Sequence: 1 LRALLTAPRSLRRSS 15

Scoring table: PAM 150
Gap 15

Searched: 106580 seqs, 10152877 residues

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database: a-issued
1:5A_COMB 2:5B_COMB 3:PCT9_COMB 4:backfiles1

Statistics: Mean 17.828; Variance 71.575; scale 0.249

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES				Pred. No.	
Result No.	Score	Query Match	Description	Pred. No.	
1	101	100.0	Sequence 2, Applicatio	8.81e-03	
2	101	100.0	Patent No. 5212286-4	8.81e-03	
3	101	100.0	Patent No. 5212286-2	8.81e-03	
4	95	94.1	Patent No. 5212286-6	3.21e-02	
5	79	78.2	Patent No. 5202239-3	9.45e-01	
6	79	78.2	Patent No. 5202239-1	9.45e-01	
7	64	63.4	Patent No. 5449751-4	2.01e+01	
8	64	63.4	Patent No. 5449751-1	2.01e+01	
9	64	63.4	Patent No. 5449751-3	2.01e+01	
10	64	63.4	Sequence 2, Applicatio	2.01e+01	
11	64	63.4	Sequence 15, Applicati	2.01e+01	
12	64	63.4	Sequence 18, Applicati	2.01e+01	
13	64	63.4	Sequence 4, Applicatio	2.01e+01	
14	64	63.4	Sequence 15, Applicati	2.01e+01	
15	64	63.4	Sequence 5, Applicatio	2.01e+01	
16	64	63.4	Sequence 5, Applicatio	2.01e+01	
17	64	63.4	Sequence 2, Applicatio	2.01e+01	
18	64	63.4	Sequence 15, Applicati	2.01e+01	
19	64	63.4	Sequence 5, Applicatio	2.01e+01	
20	63	62.4	Sequence 3, Applicatio	2.45e+01	
21	60	59.4	Sequence 25, Applicati	4.42e+01	
22	59	58.4	Patent No. 5475095-2	5.37e+01	
23	59	58.4	Patent No. 5217865-2	5.37e+01	

24	57	56.4	2199	3	PCT-US95-1	Sequence 2, Applicatio	7.92e+01
25	55	54.5	30	4	5202239-9	Patent No. 5202239.	1.16e+02
26	55	54.5	134	1	US-08-463-	Sequence 8, Applicatio	1.16e+02
27	55	54.5	134	2	US-08-463-	Sequence 8, Applicatio	1.16e+02
28	54	53.5	577	1	US-08-484-	Sequence 24, Applicati	1.41e+02
29	54	53.5	577	1	US-08-484-	Sequence 24, Applicati	1.41e+02
30	54	53.5	695	4	5460961-5	Patent No. 5460961.	1.41e+02
31	54	53.5	3491	2	US-07-642-	Sequence 2, Applicatio	1.41e+02
32	53	52.5	107	1	US-08-399-	Sequence 5, Applicatio	1.70e+02
33	53	52.5	107	2	US-08-433-	Sequence 5, Applicatio	1.70e+02
34	53	52.5	107	2	US-08-434-	Sequence 5, Applicatio	1.70e+02
35	53	52.5	277	1	US-08-375-	Sequence 5, Applicatio	1.70e+02
36	53	52.5	277	2	US-08-752-	Sequence 5, Applicatio	1.70e+02
37	53	52.5	824	1	US-08-221-	Sequence 3, Applicatio	1.70e+02
38	53	52.5	857	3	PCT-US96-1	Sequence 2, Applicatio	1.70e+02
39	53	52.5	857	2	US-08-659-	Sequence 2, Applicatio	1.70e+02
40	53	52.5	984	3	PCT-US95-0	Sequence 19, Applicati	1.70e+02
41	53	52.5	3077	4	5223423-2	Patent No. 5223423.	1.70e+02
42	52	51.5	1810	3	PCT-US95-1	Sequence 4, Applicatio	2.06e+02
43	51	50.5	1162	2	US-08-663-	Sequence 15, Applicati	2.48e+02
44	51	50.5	2910	2	US-08-444-	Sequence 183, Applicat	2.48e+02
45	51	50.5	2910	2	US-08-461-	Sequence 183, Applicat	2.48e+02

ALIGNMENTS

RESULT 1

ID US-08-737-927-2 STANDARD; PRT; 15 AA.

XX xxxxxx

DT

XX Sequence 2, Application US/08737927

DE

XX Sequence 2, Application US/08737927

CC Patent No. 5767239

CC GENERAL INFORMATION:

CC APPLICANT: IMMER, Hansuelli

CC APPLICANT: FORSMANN, Wolf-Georg

CC APPLICANT: ADERMAN, Knut

CC APPLICANT: KLESSEN, Christian

CC TITLE OF INVENTION: PROCESS AND INTERMEDIATE PRODUCTS FOR

CC TITLE OF INVENTION: PREPARING CARDIOTILATIN FRAGMENTS, AND HIGHLY PURIF

CC TITLE OF INVENTION: CARDIOTILATIN FRAGMENTS

CC NUMBER OF SEQUENCES: 5

CC CORRESPONDENCE ADDRESS:

CC ADDRESSEE: Nikaido, Marmelstein, Murray & Oram

CC STREET: 655 Fifteenth Street N.W. Suite 330

CC CITY: Washington

CC STATE: D.C.

CC COUNTRY: U.S.A.

CC ZIP: 20005-3701

CC COMPUTER READABLE FORM:

CC MEDIUM TYPE: Floppy disk

CC COMPUTER: IBM PC compatible

CC OPERATING SYSTEM: PC-DOS/MS-DOS

CC SOFTWARE: Patentin Release #1.0, Version #1.30

CC CURRENT APPLICATION DATA:

CC APPLICATION NUMBER: US/08/737,927

CC FILING DATE:

CC CLASSIFICATION: 424

CC PRIOR APPLICATION DATA:

CC APPLICATION NUMBER: WO 95/33769

CC FILING DATE: 14-DEC-1995

CC ATTORNEY/AGENT INFORMATION:

CC NAME: Kitts, Monica C.

CC REGISTRATION NUMBER: 36,105

CC REFERENCE/DOCKET NUMBER: P1614-6052

CC TELECOMMUNICATION INFORMATION:

CC TELEPHONE: (202)638-5000

CC TELEFAX: (202)638-4810

CC INFORMATION FOR SEQ ID NO: 2:

CC SEQ ID NO:3:
CC LENGTH: 144
SQ SEQUENCE 156 AA; 17115 MW; 129665 CN;

Query Match 78.28; Score 79; DB 4; Length 144;
Best Local Similarity 91.7%; Pred. No. 9.45e-01;
Matches 11; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Db 106 LRALLTAPRSLK 117
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QY 1 LRALLTAPRSLR 12

RESULT 6
ID 5202239-1 STANDARD; PRT; 156 AA.
XX
AC xxxxxx
XX
DT 01-JAN-1900
XX
DE Patent No. 5202239.
XX
CC Patent No. 5202239
CC APPLICANT: TARNOWSKI, JOSEPH S.; HILLIKER, SANDRA; WILLETT,
CC SCOTT W.
CC TITLE OF INVENTION: EXPRESSION OF RECOMBINANT POLYPEPTIDES
CC WITH IMPROVED PURIFICATION
CC NUMBER OF SEQUENCES: 16
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: US/08/564,259
CC FILING DATE: 07-AUG-1990
CC SEQ ID NO:1:
CC LENGTH: 144
SQ SEQUENCE 156 AA; 17116 MW; 129679 CN;

Query Match 78.28; Score 79; DB 4; Length 144;
Best Local Similarity 91.7%; Pred. No. 9.45e-01;
Matches 11; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Db 106 LRALLTAPRSLK 117
| | | | | | | | | |
QY 1 LRALLTAPRSLR 12

RESULT 7
ID 5449751-4 STANDARD; PRT; 17 AA.
XX
AC xxxxxx
XX
DT 01-JAN-1900
XX
DE Patent No. 5449751.
XX
CC Patent No. 5449751
CC APPLICANT: FORSSMANN, WOLF-GEORG; ALT, JEANETTE M.; BECKER,
CC GERHARD; HERBST, FRANZ
CC TITLE OF INVENTION: CARDIODILATIN FRAGMENT, PROCESS FOR
CC PREPARING SAME AND USE THEREOF
CC NUMBER OF SEQUENCES: 4
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: US/08/185,240
CC FILING DATE: 24-JAN-1994
CC APPLICATION NUMBER: 994,084
CC FILING DATE: 16-DEC-1992
CC APPLICATION NUMBER: 795,248
CC FILING DATE: 18-NOV-1991
CC APPLICATION NUMBER: 401,401
CC FILING DATE: 01-SEP-1989
CC APPLICATION NUMBER: 100,144
CC FILING DATE: 28-AUG-1987
CC SEQ ID NO:4:
CC LENGTH: 16

SQ SEQUENCE 17 AA; 1892 MW; 1532 CN;

Query Match 63.4%; Score 64; DB 4; Length 16;
Best Local Similarity 100.0%; Pred. No. 2.01e-01;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 1 TAPRSLRRSS 10
| | | | | | | | | |
QY 6 TAPRSLRRSS 15

RESULT 8
ID 5449751-1 STANDARD; PRT; 35 AA.
XX
AC xxxxxx
XX
DT 01-JAN-1900
XX
DE Patent No. 5449751.
XX
CC Patent No. 5449751
CC APPLICANT: FORSSMANN, WOLF-GEORG; ALT, JEANETTE M.; BECKER,
CC GERHARD; HERBST, FRANZ
CC TITLE OF INVENTION: CARDIODILATIN FRAGMENT, PROCESS FOR
CC PREPARING SAME AND USE THEREOF
CC NUMBER OF SEQUENCES: 4
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: US/08/185,240
CC FILING DATE: 24-JAN-1994
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: 994,084
CC FILING DATE: 16-DEC-1992
CC APPLICATION NUMBER: 795,248
CC FILING DATE: 18-NOV-1991
CC APPLICATION NUMBER: 401,401
CC FILING DATE: 01-SEP-1989
CC APPLICATION NUMBER: 100,144
CC FILING DATE: 28-AUG-1987
CC SEQ ID NO:1:
CC LENGTH: 32
SQ SEQUENCE 35 AA; 3838 MW; 6483 CN;

Query Match 63.4%; Score 64; DB 4; Length 32;
Best Local Similarity 100.0%; Pred. No. 2.01e-01;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 1 TAPRSLRRSS 10
| | | | | | | | | |
QY 6 TAPRSLRRSS 15

RESULT 9
ID 5449751-3 STANDARD; PRT; 35 AA.
XX
AC xxxxxx
XX
DT 01-JAN-1900
XX
DE Patent No. 5449751.
XX
CC Patent No. 5449751
CC APPLICANT: FORSSMANN, WOLF-GEORG; ALT, JEANETTE M.; BECKER,
CC GERHARD; HERBST, FRANZ
CC TITLE OF INVENTION: CARDIODILATIN FRAGMENT, PROCESS FOR
CC PREPARING SAME AND USE THEREOF
CC NUMBER OF SEQUENCES: 4
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: US/08/185,240
CC FILING DATE: 24-JAN-1994
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: 994,084
CC FILING DATE: 16-DEC-1992
CC APPLICATION NUMBER: 795,248

CC FILING DATE: 18-NOV-1991
CC APPLICATION NUMBER: 401,401
CC FILING DATE: 01-SEP-1989
CC APPLICATION NUMBER: 100,144
CC FILING DATE: 28-AUG-1987
CC SEQ ID NO:3
CC LENGTH: 32
SQ SEQUENCE 35 AA; 3838 MW; 6483 CN;

Query Match 63.4%; Score 64; DB 4; Length 32;
Best Local Similarity 100.0%; Pred. No. 2.01e+01;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 1 TAPRSLRRSS 10
QY 6 TAPRSLRRSS 15
|||||

RESULT 10
ID PCT-US94-12591-2 STANDARD; PRT; 32 AA.

XX XXXXXX

Sequence 2, Application PC/TUS9412591

Sequence 2, Application PC/TUS9412591

GENERAL INFORMATION:

APPLICANT: Genentech, Inc.

APPLICANT: Lowe, David

APPLICANT: Cunningham, Brian C.

APPLICANT: Oare, David

APPLICANT: McDowell, Robert S.

APPLICANT: Burnier, John

TITLE OF INVENTION: RECEPTOR SPECIFIC ATRIAL NATRIURETIC

PEPTIDES

NUMBER OF SEQUENCES: 47

CORRESPONDENCE ADDRESS:

ADDRESSEE: Genentech, Inc.

STREET: 460 Point San Bruno Blvd

CITY: South San Francisco

STATE: California

COUNTRY: USA

ZIP: 94080

COMPUTER READABLE FORM:

MEDIUM TYPE: 5.25 inch, 360 kb floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: patin (Genentech)

CURRENT APPLICATION DATA:

APPLICATION NUMBER: PCT/US94/12591

FILING DATE:

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/152994

FILING DATE: 12-NOV-1993

ATTORNEY/AGENT INFORMATION:

NAME: Winter, Daryl B.

REGISTRATION NUMBER: 32,637

REFERENCE/DOCKET NUMBER: 844P1

TELECOMMUNICATION INFORMATION:

TELEPHONE: 415/952-9881

TELEFAX: 415/952-9881

TELEX: 910/371-7168

INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:

LENGTH: 32 amino acids

TYPE: amino acid

TOPOLOGY: linear

SEQUENCE 32 AA; 3508 MW; 4652 CN;

Query Match 63.4%; Score 64; DB 3; Length 32;

Best Local Similarity 100.0%; Pred. No. 2.01e+01;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 1 TAPRSLRRSS 10
QY 6 TAPRSLRRSS 15
|||||

RESULT 11
ID US-08-470-846A-15 STANDARD; PRT; 32 AA.

XX XXXXXX

Sequence 15, Application US/08470846A

Sequence 15, Application US/08470846A

Patent No. 5846932

GENERAL INFORMATION:

APPLICANT: Genentech, Inc.

APPLICANT: Lowe, David G.

APPLICANT: Cunningham, Brian C.

APPLICANT: Oare, David

APPLICANT: McDowell, Robert S.

APPLICANT: Burnier, John

TITLE OF INVENTION: RECEPTOR SPECIFIC ATRIAL NATRIURETIC

PEPTIDES

NUMBER OF SEQUENCES: 43

CORRESPONDENCE ADDRESS:

ADDRESSEE: Genentech, Inc.

STREET: 460 Point San Bruno Blvd

CITY: South San Francisco

STATE: California

COUNTRY: USA

ZIP: 94080

COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Winpatin (Genentech)

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/470,846A

FILING DATE: 06-Jun-1995

CLASSIFICATION: 514

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/419877

FILING DATE: 11-APR-1995

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/362552

FILING DATE: 06-JAN-1995

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/152994

FILING DATE: 12-NOV-1993

ATTORNEY/AGENT INFORMATION:

NAME: Kubinec, Jeffrey S.

REGISTRATION NUMBER: 36,575

REFERENCE/DOCKET NUMBER: P0844P2C1

TELECOMMUNICATION INFORMATION:

TELEPHONE: 415/225-8228

TELEFAX: 415/952-9881

TELEX: 910/371-7168

INFORMATION FOR SEQ ID NO: 15:

SEQUENCE CHARACTERISTICS:

LENGTH: 32 amino acids

TYPE: Amino Acid

TOPOLOGY: Linear

SEQUENCE 32 AA; 3564 MW; 4811 CN;

Query Match 63.4%; Score 64; DB 2; Length 32;

Best Local Similarity 100.0%; Pred. No. 2.01e+01;

Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 1 TAPRSLRRSS 10

CC Sequence 15, Application PC/TUS9412591
CC GENERAL INFORMATION:
CC APPLICANT: Genentech, Inc.
CC APPLICANT: Lowe, David
CC APPLICANT: Cunningham, Brian C.
CC APPLICANT: Oare, David
CC APPLICANT: McDowell, Robert S.
CC APPLICANT: Burnier, John
CC TITLE OF INVENTION: RECEPTOR SPECIFIC ATRIAL NATRIURETIC
CC TITLE OF INVENTION: PEPTIDES
CC NUMBER OF SEQUENCES: 47
CC CORRESPONDENCE ADDRESS:
CC ADDRESSEE: Genentech, Inc.
CC STREET: 460 Point San Bruno Blvd
CC CITY: South San Francisco
CC STATE: California
CC COUNTRY: USA
CC ZIP: 94080
CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
CC COMPUTER: IBM PC compatible
CC OPERATING SYSTEM: PC-DOS/MS-DOS
CC SOFTWARE: patin (Genentech)
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: PCT/US94/12591
CC FILING DATE:
CC CLASSIFICATION:
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: 08/152994
CC FILING DATE: 12-NOV-1993
CC ATTORNEY/AGENT INFORMATION:
CC NAME: Winter, Daryl B.
CC REGISTRATION NUMBER: 32,637
CC REFERENCE/DOCKET NUMBER: 844P1
CC TELEPHONE: 415/225-1249
CC TELEFAX: 415/952-9881
CC TELEX: 910/371-7168
CC INFORMATION FOR SEQ ID NO: 15:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 32 amino acids
CC TYPE: amino acid
CC TOPOLOGY: linear
CC SEQUENCE 32 AA: 3564 MW; 4811 CN;
Query Match 63.4%; Score 64; DB 3; Length 32;
Best Local Similarity 100.0%; Pred. No. 2.01e+01;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Db 1 TAPRSLRRSS 10
QY 6 TAPRSLRRSS 15
RESULT 15
ID PCT-US94-12591-5 STANDARD; PRT: 32 AA.
XX
AC xxxxxx
XX
DT
XX
DE Sequence 5, Application PC/TUS9412591
XX
CC GENERAL INFORMATION:
CC APPLICANT: Genentech, Inc.
CC APPLICANT: Lowe, David
CC APPLICANT: Cunningham, Brian C.
CC APPLICANT: Oare, David
CC APPLICANT: McDowell, Robert S.
CC APPLICANT: Burnier, John
CC TITLE OF INVENTION: RECEPTOR SPECIFIC ATRIAL NATRIURETIC
CC TITLE OF INVENTION: PEPTIDES

CC NUMBER OF SEQUENCES: 47
CC CORRESPONDENCE ADDRESS:
CC ADDRESSEE: Genentech, Inc.
CC STREET: 460 Point San Bruno Blvd
CC CITY: South San Francisco
CC STATE: California
CC COUNTRY: USA
CC ZIP: 94080
CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
CC COMPUTER: IBM PC compatible
CC OPERATING SYSTEM: PC-DOS/MS-DOS
CC SOFTWARE: patin (Genentech)
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: PCT/US94/12591
CC FILING DATE:
CC CLASSIFICATION:
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: 08/152994
CC FILING DATE: 12-NOV-1993
CC ATTORNEY/AGENT INFORMATION:
CC NAME: Winter, Daryl B.
CC REGISTRATION NUMBER: 32,637
CC REFERENCE/DOCKET NUMBER: 844P1
CC TELEPHONE: 415/225-1249
CC TELEFAX: 415/952-9881
CC TELEX: 910/371-7168
CC INFORMATION FOR SEQ ID NO: 5:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 32 amino acids
CC TYPE: amino acid
CC TOPOLOGY: linear
CC SEQUENCE 32 AA: 3589 MW; 4484 CN;
Query Match 63.4%; Score 64; DB 3; Length 32;
Best Local Similarity 100.0%; Pred. No. 2.01e+01;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 6 TAPRSLRRSS 15
Search completed: Wed Jun 16 13:21:08 1999
Job time : 7 secs.

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2	101	100.0	152	1	ANBO		atrial natriuretic pe	1.10e-07
3	101	100.0	153	1	AWRB		atrial natriuretic pe	1.10e-07
4	98	97.0	149	1	AWDG		atrial natriuretic pe	4.64e-07
5	98	97.0	150	1	S13107		atrial natriuretic pe	4.64e-07
6	98	97.0	153	2	S14873		atrial natriuretic pe	4.64e-07
7	95	94.1	128	2	S14872		atrial natriuretic pe	1.92e-06
8	95	94.1	152	1	AWRT		atrial natriuretic fa	1.92e-06
9	95	94.1	152	1	AWWS		atrial natriuretic pe	1.92e-05
10	88	87.1	145	2	J00947		atrial natriuretic pe	4.96e-05
11	66	65.3	758	2	S17148		lethal(2)denticleless	6.56e-01
12	65	64.4	196	2	E90100		hypothetical protein	9.77e-01
13	61	60.4	215	2	G70575		hypothetical protein	4.63e+00
14	61	60.4	860	2	S55543		reverse transcriptase	4.63e+00
15	60	59.4	217	2	D64935		hypothetical protein	6.76e+00
16	59	58.4	102	2	E5040		hypothetical protein.	9.83e+00
17	59	58.4	102	2	C64007		hypothetical protein	9.83e+00
18	59	58.4	296	2	A40593		transcription activat	9.83e+00
19	59	58.4	529	1	A0HUBA		beta-N-acetylhexosami	9.83e+00
20	59	58.4	649	2	J01515		dnak-type molecular c	9.83e+00
21	58	57.4	341	2	S26206		hypothetical protein	1.42e+01
22	58	57.4	528	2	I48253		beta-N-acetylhexosami	1.42e+01
23	58	57.4	655	2	A42420		L-iduronidase (EC 3.2	1.42e+01


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REFERENCE
A32733
#authors Kangawa, K.; Matsuo, H.
#journal Biochem. Biophys. Res. Commun. (1984) 118:131-139
#title Purification and complete amino acid sequence of alpha-human
atrial natriuretic polypeptide (alpha-hANP).
#cross-references MUID:84128019
#accession A32733
#molecule_type protein
#residues 124-151 ##label KAN
REFERENCE
I58054
#authors Nakayama, K.; Ohkubo, H.; Hirose, T.; Inayama, S.; Nakanishi, S.
#journal Nature (1984) 310:699-701
#title mRNA sequence for human cardiodilatin-atrial natriuretic
factor precursor and regulation of precursor mRNA in rat
atria.
#cross-references MUID:84295577
#accession I58054
#molecule_type mRNA
#residues 1-151 ##label RES
##cross-references GB:M30262; NID:g180181; PID:g180182
REFERENCE
S14097
#authors Vanneste, Y.; Michel, A.; Deschodt-Lancman, M.
#journal Eur. J. Biochem. (1991) 196:281-286
#title Hydrolysis of intact and Cys-Phe-cleaved human atrial
natriuretic peptide in vitro by human tissue kallikrein.
#cross-references MUID:91176998
#accession S14097
#molecule_type protein
#residues 124-151 ##label VAN
#note natural and synthetic peptide subjected to kallikrein
proteolysis
REFERENCE
I39458
#authors Zivin, R.A.; Condra, J.H.; Dixon, R.A.; Seidah, N.G.;
Chretien, M.; Nemer, M.; Chamberland, M.; Drouin, J.
#journal Proc. Natl. Acad. Sci. U.S.A. (1984) 81:6325-6329
#title Molecular cloning and characterization of DNA sequences
encoding rat and human atrial natriuretic factors.
#cross-references MUID:85038509
#accession I39458
#status preliminary; translated from GB/EMBL/DBJ
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##cross-references GB:K02044; NID:g178631; PID:g178632
REFERENCE
I39459
#authors Maki, M.; Parmentier, M.; Inagami, T.
#journal Biochem. Biophys. Res. Commun. (1984) 125:797-802
#title Cloning of genomic DNA for human atrial natriuretic factor.
#cross-references MUID:85096983
#accession I39459
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I39460
#authors Seidman, C.E.; Bloch, K.D.; Zisfein, J.; Smit, J.; Haber, E.;
Honey, C.J.; Duby, A.D.; Choi, E.; Graham, R.M.; Seidman,
J.G.
#journal Hypertension (1985) 7:31-34
#title Molecular studies of the atrial natriuretic factor gene.
#accession I39460
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#molecule_type DNA
#residues 1-64,'D',66-151 ##label RE4
##cross-references GB:M54951; NID:g178636; PID:g178638
REFERENCE
I37167
#authors Greenberg, B.D.; Bencen, G.H.; Seilhamer, J.J.; Lewicki,
J.A.; Fiddes, J.C.
#journal Nature (1984) 312:656-658

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#title Nucleotide sequence of the gene encoding human atrial
natriuretic factor precursor.
#cross-references MUID:85061627
#accession I37167
#status translated from GB/EMBL/DBJ
#molecule_type DNA
#residues 26-151 ##label RE5
##cross-references EMBL:X01471; NID:g28690
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natriuretic.
GENETICS
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#map_position 1p36-1p36
#introns 41/3; 150/3
CLASSIFICATION #superfamily natriuretic peptide A precursor
KEYWORDS atrium; diuretic; hormone; natriuretic; osmoregulation
FEATURE
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26-151 #product cardiodilatin #status predicted #label CDD\
124-151 #product atrial alpha natriuretic peptide #status
experimental #label ANP\
130-146 #disulfide_bonds #status experimental
SUMMARY #length 151 #molecular-weight 16395 #checksum 3644
Query Match 100.0%; Score 101; DB 1; Length 151;
Best Local Similarity 100.0%; Pred. No. 1.10e-07;
Matches 15; Conservations 0; Mismatches 0; Indels 0; Gaps 0;
Db 115 LRALLTAPRSLRRSS 129
QY 1 LRALLTAPRSLRRSS 15
|||||
RESULT 2
ENTRY AWBO #type complete
TITLE atrial natriuretic peptide precursor - bovine
ALTERNATE_NAMES ANP; atrial natriuretic polypeptide
ORGANISM #formal_name Bos primigenius taurus #common_name cattle
DATE 30-Jun-1989 #sequence_revision 30-Jun-1989 #text_change
20-Mar-1998
ACCESSIONS A90124; A93049; A24247; A26090
REFERENCE A90124
#authors Vlasuk, G.P.; Miller, J.; Bencen, G.H.; Lewicki, J.A.
#journal Biochem. Biophys. Res. Commun. (1986) 136:396-403
#title Structure and analysis of the bovine atrial natriuretic
peptide precursor gene.
#cross-references MUID:85215205
#accession A90124
#molecule_type DNA
#residues 1-152 ##label VLA
##cross-references GB:M13145; NID:g162665; PID:g162666
REFERENCE A93049
#authors Ong, H.; McNicoll, N.; Lazure, C.; Seidah, N.; Chretien, M.;
Cantin, M.; De Lean, A.
#journal Life Sci. (1986) 38:1309-1315
#title Purification and sequence determination of bovine atrial
natriuretic factor.
#cross-references MUID:85173941
#accession A93049
#molecule_type protein
#residues 123-150 ##label ONG
GENETICS
#introns 40/3; 149/3
CLASSIFICATION #superfamily natriuretic peptide A precursor
KEYWORDS atrium; diuretic; hormone; natriuretic; osmoregulation
FEATURE
1-24 #domain signal sequence #status predicted #label SIG\
25-152 #product gamma atrial natriuretic factor #status
predicted #label ANP\
123-150 #product alpha atrial natriuretic peptide #status
experimental #label ANP\
129-145 #disulfide_bonds #status predicted

```

```

SUMMARY          #length 152 #molecular-weight 16518 #checksum 7552

Query Match      100.0%; Score 101; DB 1; Length 152;
Best Local Similarity 100.0%; Pred. No. 1.10e-07;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 114 LRALLTAPRSLRRSS 128
|||||
QY 1 LRALLTAPRSLRRSS 15

RESULT 3
ENTRY ANRP #type complete
TITLE atrial natriuretic peptide precursor - rabbit
ALTERNATE_NAMES ANP; atrial natriuretic polypeptide
ORGANISM #formal_name Oryctolagus cuniculus #common_name domestic
rabbit
DATE 31-Mar-1988 #sequence_revision 31-Mar-1988 #text_change
20-Mar-1998
ACCESSIONS B25302
REFERENCE A90119
AUTHORS Oikawa, S.; Imai, M.; Inuzuka, C.; Tawaragi, Y.; Nakazato,
H.; Matsuo, H.
#journal Biochem. Biophys. Res. Commun. (1985) 132:892-899
#title Structure of dog and rabbit precursors of atrial natriuretic
polypeptides deduced from nucleotide sequence of cloned
cDNA.
#cross-references MUID:86076957
#accession B25302
#molecule_type mRNA
#residues 1-153 #label OIK
#cross-references GB:M12046; NID:g164770; PID:g164771
CLASSIFICATION #superfamily natriuretic peptide A precursor
KEYWORDS atrium; diuretic; hormone; natriuretic; osmoregulation
FEATURE
1-25 #domain signal sequence #status predicted #label SIG\
26-151 #product gamma atrial natriuretic factor #status
predicted #label ANF\
124-151 #product alpha atrial natriuretic peptide #status
predicted #label ANP\
130-146 #disulfide_bonds #status predicted
SUMMARY #length 133 #molecular-weight 16843 #checksum 7650

Query Match      100.0%; Score 101; DB 1; Length 153;
Best Local Similarity 100.0%; Pred. No. 1.10e-07;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 115 LRALLTAPRSLRRSS 129
|||||
QY 1 LRALLTAPRSLRRSS 15

RESULT 4
ENTRY AWDG #type complete
TITLE atrial natriuretic peptide precursor - dog
ALTERNATE_NAMES ANP; atrial natriuretic polypeptide
ORGANISM #formal_name Canis lupus familiaris #common_name dog
DATE 31-Mar-1988 #sequence_revision 31-Mar-1988 #text_change
22-Jan-1999
ACCESSIONS A25302
REFERENCE A90119
AUTHORS Oikawa, S.; Imai, M.; Inuzuka, C.; Tawaragi, Y.; Nakazato,
H.; Matsuo, H.
#journal Biochem. Biophys. Res. Commun. (1985) 132:892-899
#title Structure of dog and rabbit precursors of atrial natriuretic
polypeptides deduced from nucleotide sequence of cloned
cDNA.
#cross-references MUID:86076957
#accession A25302
#molecule_type mRNA
#residues 1-149 #label OIK
#cross-references GB:M12045; NID:g163900; PID:g163901
CLASSIFICATION #superfamily natriuretic peptide A precursor

```

```

atrium; diuretic; hormone; natriuretic; osmoregulation

#domain signal sequence #status predicted #label SIG\
#product gamma atrial natriuretic factor #status
predicted #label ANF\
#product alpha atrial natriuretic peptide #status
predicted #label ANP\
#disulfide_bonds #status predicted
#length 149 #molecular-weight 15819 #checksum 8040

Query Match          97.0%; Score 98; DB 1; Length 149;
Best Local Similarity 93.3%; Pred. No. 4.64e-07;
Matches 14; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Db 113 LRALLAAPRLRRSS 127
      |||||:|||||
Qy 1 LRALLTAPRLRRSS 15

RESULT 5
ENTRY SL13107 #type complete
TITLE atrial natriuretic peptide precursor - pig
CONTAINS alpha atrial natriuretic peptide; gamma atrial natriuretic
factor (cardiolipatin)
ORGANISM #formal_name Sus scrofa domestica #common_name domestic pig
DATE 21-Nov-1993 #sequence_revision 14-Jul-1994 #text_change
20-Mar-1998
ACCESSIONS SL13107; A60899
REFERENCE SL13107
#authors Maegert, H.J.; Appelhans, H.; Gassen, H.G.; Forssmann, W.G.
#journal Nucleic Acids Res. (1990) 18:6704
#title Nucleotide sequence of a porcine prepro atrial natriuretic
peptide (ANP) cDNA.
#cross-references MUID:91067478
#accession SL13107
#molecule_type mRNA
#residues 1-150 #label MAE
#cross-references EMBL:X54669; NID:g1883; PID:g1884
REFERENCE A60899
#authors Forssmann, W.G.; Hock, D.; Lottspeich, A.; Henschen, A.;
Kreye, V.; Christmann, M.; Reinecke, M.; Metz, J.;
Carlsquist, M.; Mutt, V.
#journal Anat. Embryol. (1983) 168:307-313
#title The right auricle of the heart is an endocrine organ.
Cardiolipatin as a peptide hormone candidate.
#accession A60899
#molecule_type protein
#residues 25-54 #label FOR
CLASSIFICATION #superfamily natriuretic peptide A precursor
KEYWORDS atrium; diuretic; hormone; natriuretic; osmoregulation
FEATURE
1-24 #domain signal sequence #status predicted #label SIG\
25-150 #product gamma atrial natriuretic factor #status
predicted #label ANF\
#product alpha atrial natriuretic peptide #status
predicted #label ANP\
#disulfide_bonds #status predicted
#length 150 #molecular-weight 16351 #checksum 9859

Query Match          97.0%; Score 98; DB 1; Length 150;
Best Local Similarity 93.3%; Pred. No. 4.64e-07;
Matches 14; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Db 114 LRALLAAPRLRRSS 128
      |||||:|||||
Qy 1 LRALLTAPRLRRSS 15

RESULT 6
ENTRY SL14873 #type complete
TITLE atrial natriuretic peptide precursor - horse
ORGANISM #formal_name Equus caballus #common_name domestic horse
DATE 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change

```

```

08-Sep-1997
SI4873
#accessions
SI4872
#reference
Maegert, H.J.; Hanke, M.; Schmieding, G.; Teuteberg, K.;
Schulz-Knappe, P.; Forssmann, W.G.
#authors
submitted to the EMBL Data Library, March 1991
#submission
SI4873
#accession
#status preliminary
#molecule_type mRNA
#residues 1-153 #label MAE
#cross-references EMBL:X58563; NID:g1008; PID:g1009
CLASSIFICATION superfamily natriuretic peptide A precursor
SUMMARY #length 153 #molecular-weight 16825 #checksum 960

Query Match 97.0%; Score 98; DB 2; Length 153;
Best Local Similarity 93.3%; Pred. NO. 4.64e-07;
Matches 14; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Db 115 LRALLAAPSRLRSS 129
QY 1 LRALLTAPSLRSS 15

RESULT 7
ENTRY #type fragment
TITLE atrial natriuretic peptide precursor - guinea pig (fragment)
ORGANISM #formal_name Cavia porcellus #common_name guinea pig
DATE 20-Feb-1995 #sequence_revision 30-Jan-1998 #text_change
20-Mar-1998
ACCESSIONS SI4872
REFERENCE SI4872
#authors Maegert, H.J.; Hanke, M.; Schmieding, G.; Teuteberg, K.;
Schulz-Knappe, P.; Forssmann, W.G.
#submission submitted to the EMBL Data Library, March 1991
#accession SI4872
#molecule_type mRNA
#residues 1-128 #label MAE
#cross-references EMBL:X58563; NID:g49543; PID:g49544
#experimental_source heart atria; adult
CLASSIFICATION superfamily natriuretic peptide A precursor
KEYWORDS atrium; diuretic; hormone; natriuretic; osmoregulation
FEATURE 1-98
99-128 #domain signal sequence #status predicted #label SIG\
#product atrial natriuretic peptide #status predicted
#label MAT\
105-121 #disulfide_bonds #status predicted
SUMMARY #length 128 #checksum 8741

Query Match 94.1%; Score 95; DB 2; Length 128;
Best Local Similarity 93.3%; Pred. NO. 1.92e-06;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Db 90 LRALLDAPSLRSS 104
QY 1 LRALLTAPSLRSS 15

RESULT 8
ENTRY #type complete
TITLE atrial natriuretic factor precursor - rat
CONTAINS ANF(1-33); ANF(2-33); ANF(3-33); ANF(8-33); atrial
natriuretic peptide; atriopeptin I; atriopeptin II;
auriculin A; auriculin B; preprocardionatin
ORGANISM #formal_name Rattus norvegicus #common_name Norway rat
DATE 19-Feb-1984 #sequence_revision 15-Nov-1984 #text_change
26-Feb-1999
ACCESSIONS A22570; A01425; A93332; A43617; A93330; A94275; PT0061;
A20973; A44190; A60390; I59094; I58057; I52678
REFERENCE A22570
#authors Argentin, S.; Nemer, M.; Drouin, J.; Scott, G.K.; Kennedy,
B.P.; Davies, P.L.
#journal J. Biol. Chem. (1985) 260:4568-4571
#title The gene for rat atrial natriuretic factor.

#cross-references MUID:85182558
#accession A22570
#molecule_type DNA
#residues 1-152 #label ARG
#cross-references GB:K02062; NID:g202899; PID:g202900
REFERENCE A93331
#authors Yamanaka, M.; Greenberg, B.; Johnson, L.; Seilhamer, J.;
Brewer, M.; Friedenmann, T.; Miller, J.; Atlas, S.; Laragh,
J.; Lewicki, J.; Fiddes, J.
#journal Nature (1984) 309:719-722
#title Cloning and sequence analysis of the cDNA for the rat atrial
natriuretic factor precursor.
#cross-references MUID:84219797
#accession A01425
#molecule_type mRNA
#residues 1-152 #label YAM
#cross-references EMBL:X00665; NID:g55711; PID:g55712
REFERENCE A93332
#authors Maki, M.; Takayanagi, R.; Misono, K.S.; Pandey, K.N.;
Tibbetts, C.; Inagami, T.
#journal Nature (1984) 309:722-724
#title Structure of rat atrial natriuretic factor precursor deduced
from cDNA sequence.
#cross-references MUID:84219798
#accession A93332
#molecule_type mRNA
#residues 1-152 #label MAK
#cross-references GB:X00665; EMBL:X00658; NID:g55711; PID:g55712
REFERENCE A43617
#authors Seidman, C.E.; Duby, A.D.; Choi, E.; Graham, R.M.; Haber, E.;
Hovey, C.; Smith, J.A.; Seidman, J.G.
#journal Science (1984) 225:324-326
#title The structure of rat preproatrial natriuretic factor as
defined by a complementary DNA clone.
#cross-references MUID:84250178
#accession A43617
#molecule_type mRNA
#residues 1-152 #label SEI
#cross-references GB:K02062; GB:K02063; NID:g202899; PID:g202900
REFERENCE A93330
#authors Atlas, S.A.; Kleinert, H.D.; Camargo, M.J.; Januszewicz, A.;
Sealey, J.E.; Laragh, J.H.; Schilling, J.W.; Lewicki, J.A.;
Johnson, L.K.; Maack, T.
#journal Nature (1984) 309:717-719
#title Purification, sequencing and synthesis of natriuretic and
vasoactive rat atrial peptide.
#cross-references MUID:84219796
#accession A93330
#molecule_type protein
#residues 126-149 #label ATL
REFERENCE A94275
#authors Currie, M.G.; Geller, D.M.; Cole, B.R.; Siegel, N.R.; Fok,
K.F.; Adams, S.P.; Eubanks, S.R.; Galluppi, G.R.;
Needleman, P.
#journal Science (1984) 223:67-69
#title Purification and sequence analysis of bioactive atrial
peptides (atriopeptins).
#cross-references MUID:84097513
#accession A94275
#molecule_type protein
#residues 127-149 #label CUR
REFERENCE PT0061
#authors Thibault, G.; Murthy, K.K.; Gutkowska, J.; Seidah, N.G.;
Lazure, C.; Chretien, M.; Cantin, M.
#journal Peptides (1988) 9:47-53
#title NH2-terminal fragment of rat pro-atrial natriuretic factor in
the circulation: identification, radioimmunoassay and
half-life.
#cross-references MUID:88203350
#accession PT0061
#molecule_type protein
#residues 25-28; 'X', 30-31; 'X', 33; 'X', 35-38 #label THI
REFERENCE A20973

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#authors      Seidah, N.G.; Lazure, C.; Chretien, M.; Thibault, G.; Garcia,
               R.; Cantin, M.; Genest, J.; Nutt, R.F.; Brady, S.F.; Lyle,
               T.A.; Paleveda, W.J.; Colton, C.D.; Ciccarone, T.M.; Veber,
               D.F.
#journal      Proc. Natl. Acad. Sci. U.S.A. (1984) 81:2640-2644
#title        Amino acid sequence of homologous rat atrial peptides:
               natriuretic activity of native and synthetic forms.
#cross-references MUID:84194062
#accession     A20973
#molecule_type protein
#residues      118-150 ##label SE2
REFERENCE
#authors      Flynn, T.G.; Davies, P.L.; Kennedy, B.P.; de Boid, M.L.; de
               Boid, A.J.
#journal      Science (1985) 228:323-325
#title        Alignment of rat cardionatrin sequences with the
               preprocardionatrin sequence from complementary DNA.
#cross-references MUID:85168263
#accession     A44190
#molecule_type mRNA
#residues      1-152 ##label FLY
#cross-references GB:K02062; NID:g202899; PID:g202900
#note         part of this sequence, including the amino ends of three
               mature peptides, was confirmed by protein sequencing
REFERENCE
#authors      Belcourt, D.; Varma, D.R.; Toney, K.; Bennett, H.P.J.
               Protein Expr. Purif. (1990) 1:28-32
#journal      Purification of rat pro-atrial natriuretic factor: a
               simplified scheme using reversed-phase high-performance
               liquid chromatography.
#cross-references MUID:93044510
#accession     A60390
#molecule_type protein
#residues      25-39 ##label BEL
REFERENCE
#authors      Gardner, D.G.; Vlasuk, G.P.; Baxter, J.D.; Fiddes, J.C.;
               Lewicki, J.A.
#journal      Proc. Natl. Acad. Sci. U.S.A. (1987) 84:2175-2179
#title        Identification of atrial natriuretic factor gene transcripts
               in the central nervous system of the rat.
#cross-references MUID:87175636
#accession     I59094
#molecule_type mRNA
#status        translated from GB/EMBL/DBJ
#residues      38-152 ##label RES
#cross-references GB:M15868; NID:g202903; PID:g202904
REFERENCE
#authors      Kangawa, K.; Tawaragi, Y.; Oikawa, S.; Mizuno, A.;
               Sakuragawa, Y.; Nakazato, H.; Fukuda, A.; Minamino, N.;
               Matsuo, H.
#journal      Nature (1984) 312:152-155
#title        Identification of rat gamma atrial natriuretic polypeptide
               and characterization of the cDNA encoding its precursor.
#cross-references MUID:85061500
#accession     I58057
#molecule_type mRNA
#status        preliminary; translated from GB/EMBL/DBJ
#residues      1-152 ##label RE2
#cross-references EMBL:X01118; NID:g55716; PID:g55717
REFERENCE
#authors      Flynn, T.G.
#journal      Can. J. Physiol. Pharmacol. (1987) 65:2013-2020
#title        The elucidation of the structure of atrial natriuretic
               factor, a new peptide hormone.
#cross-references MUID:88109092
#accession     I52678
#molecule_type mRNA
#status        preliminary; translated from GB/EMBL/DBJ
#residues      1-51,'X',53-85,'X',87-152 ##label RE3
#cross-references GB:M27498; NID:g202905; PID:g202906
COMMENT       A disulfide bond is required for full activity of atriopeptins.
               Several active peptides may be derived from the carboxyl region of
               this precursor.
GENETICS
#gene         ANF
#introns      40/3; 149/3
CLASSIFICATION
#superfamily  natriuretic peptide A precursor
#diuretic; hormone; natriuretic; osmoregulation
KEYWORDS
#domain signal sequence #status predicted #label SIG\
#product pro-atrial natriuretic factor #status
               experimental #label PRO\
#product cardionatrin IV #status experimental #label
               CN4\
#product cardionatrin III #status experimental #label
               CN3\
#product ANF(1-33) #status experimental #label ANF1\
#product ANF(2-33) #status experimental #label ANF2\
#product ANF(3-33) #status experimental #label ANF3\
#product cardionatrin I #status experimental #label CN1\
#product ANF(8-33) #status experimental #label ANF4\
#product auriculin B #status experimental #label AUB\
#product auriculin A #status experimental #label AUA\
#product atrial natriuretic factor #status predicted
               #label MAT\
#product atriopeptin I #status experimental #label AT1\
#product atriopeptin II #status experimental #label AT2\
#disulfide_bonds #status experimental
SUMMARY
#length 152 #molecular-weight 16556 #checksum 7818
Query Match 94.1%; Score 95; DB 1; Length 152;
Best Local Similarity 86.7%; Pred.No. 1.92e-06;
Matches 13; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
Db 114 LRALLAGPSLRSS 128
||||:|||||||
QY 1 LRALLTAPSLRSS 15
||||:|||||||
RESULT 9
ENTRY AWMS #type complete
TITLE atrial natriuretic peptide precursor - mouse
ORGANISM #formal_name Mus musculus #common_name house mouse
DATE 31-Mar-1988 #sequence_revision 31-Mar-1988 #text_change
20-Mar-1998
ACCESSION A29370; B43619
REFERENCE A29370
#authors Seidman, C.E.; Bloch, K.D.; Klein, K.A.; Smith, J.A.;
               Seidman, J.G.
#journal Science (1984) 226:1206-1209
#title Nucleotide sequences of the human and mouse atrial
               natriuretic factor genes.
#cross-references MUID:85065766
#accession A29370
#molecule_type DNA
#residues      1-152 ##label SEI
#cross-references GB:K02781; NID:g191937; PID:g387099
GENETICS
#gene         ANF
#introns      40/3; 149/3
CLASSIFICATION
#superfamily  natriuretic peptide A precursor
#diuretic; hormone; natriuretic; osmoregulation
KEYWORDS
#domain signal sequence #status predicted #label SIG\
#product gamma atrial natriuretic factor #status
               predicted #label ANF\
#product alpha atrial natriuretic peptide #status
               predicted #label ANP\
#disulfide_bonds #status predicted
SUMMARY
#length 152 #molecular-weight 16645 #checksum 9384
Query Match 94.1%; Score 95; DB 1; Length 152;
Best Local Similarity 86.7%; Pred.No. 1.92e-06;
Matches 13; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
Db 114 LRALLAGPSLRSS 128
||||:|||||||

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QY 1 LRALLTAPRSLRSS 15

RESULT 10 JQ0947 #type complete
ENTRY title atrial natriuretic peptide precursor - bullfrog
ALTERNATE_NAMES ANP; atrial natriuretic factor (ANF)
CONTAINS atrial natriuretic peptide-21; atrial natriuretic peptide-24
ORGANISM #formal_name Rana catesbeiana #common_name bullfrog
DATE 30-Sep-1991 #sequence_revision 30-Sep-1991 #text_change 20-Mar-1998

ACCESSIONS JQ0947: A31510
REFERENCE JQ0947
#authors Kojima, M.
#submission submitted to JIPID, May 1991
#accession JQ0947

#molecule_type mRNA
#residues 1-145 #label KOJ

REFERENCE A31510
#authors Sakata, J.; Kangawa, K.; Matsuo, H.
#journal Biochem. Biophys. Res. Commun. (1988) 155:1338-1345
#title Identification of new atrial natriuretic peptides in frog heart.

#cross-references NUID:89025806
#accession A31510

#molecule_type protein
#residues 122-145 #label SAK

COMMENT In mammals, several active peptides may be derived from the prohormone.

CLASSIFICATION #superfamily natriuretic peptide A precursor
KEYWORDS atrium; diuretic; hormone; natriuretic; osmoregulation

FEATURE

1-23 #domain signal sequence #status predicted #label SIG\
24-121 #domain propeptide #status predicted #label PRO\
122-145 #product atrial natriuretic peptide-24 #status experimental #label M2A\
125-145 #product atrial natriuretic peptide-21 #status experimental #label M2L\
125-141 #disulfide_bonds #status predicted
SUMMARY #length 145 #molecular_weight 15934 #checksum 1892

Query Match 87.18; Score 88; DB 2; Length 145;
Best Local Similarity 80.08; Pred. No. 4.96e-05;

Matches 12; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Db 109 LRLLNAPRSMRRSS 123

QY 1 LRALLTAPRSLRSS 15

RESULT 11 S51748 #type complete
ENTRY title lethal(2)denticleless - fruit fly (Drosophila melanogaster)
ORGANISM #formal_name Drosophila melanogaster
DATE 07-May-1995 #sequence_revision 01-Sep-1995 #text_change 24-Sep-1998

ACCESSIONS S51748
REFERENCE S51748
#authors Kurzik-Dumke, U.; Neubauer, M.; Debes, A.

#submission submitted to the EMBL Data Library, December 1994
#description Identification of the novel Drosophila melanogaster heat shock gene, lethal(2)denticleless (l(2)dtl), coding for a 83 kDa protein.

#accession S51748
#status preliminary

#molecule_type DNA
#residues 1-758 #label KUR

#cross-references EMBL:X83414; NID:9603538; PID:9603539

#gene FlyBase:l(2)dtl

#introns 3/2

CLASSIFICATION #superfamily WD repeat homology

FEATURE
206-239 #domain WD repeat homology #label WD1\
349-383 #domain WD repeat homology #label WD2

SUMMARY #length 758 #molecular_weight 82351 #checksum 9172

Query Match 65.38; Score 66; DB 2; Length 758;
Best Local Similarity 61.58; Pred. No. 6.56e-01;

Matches 8; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Db 425 LRLESTPRSLKR 437

QY 1 LRALLTAPRSLRR 13

RESULT 12

ENTRY title B69100 #type complete
TITLE hypothetical protein MTH1746 - Methanobacterium

ORGANISM #formal_name Methanobacterium thermoautotrophicum

DATE 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 03-Jun-1998

ACCESSIONS B69100

REFERENCE A69000

#authors Smith, D.E.; Doucette-Stamm, L.A.; Deloughery, C.; Lee, H.;

Dubois, J.; Aldredge, T.; Bashirzadeh, R.; Blakely, D.; Cook, R.; Gilbert, K.; Harrison, D.; Hoang, L.; Keagle, P.; Lumm, W.; Pothier, B.; Qiu, D.; Spadafora, R.; Vicaire, R.; Wang, Y.; Wierzbowski, J.; Gibson, R.; Jiواني, N.; Caruso, A.; Bush, D.; Safer, H.; Patwell, D.; Prabhakar, S.; McDougall, S.; Shimer, G.; Goyal, A.; Pietrokovski, S.; Church, G.M.; Daniels, C.J.; Mao, J.; Rice, P.; Noelling, J.; Reeve, J.N.

#journal J. Bacteriol. (1997) 179:7135-7155

#title Complete genome sequence of Methanobacterium thermoautotrophicum Delta H: functional analysis and comparative genomics.

#cross-references NUID:98037514

#accession B69100

#status preliminary; nucleic acid sequence not shown;

#molecule_type DNA

#residues 1-196 #label MTH

#cross-references GB:AE000930; GB:AE000666; NID:92622872; PID:92622878

#experimental_source strain Delta H

GENETICS

#gene

MTH1746

SUMMARY #length 196 #molecular_weight 21469 #checksum 5941

Query Match 64.48; Score 65; DB 2; Length 196;
Best Local Similarity 53.38; Pred. No. 9.77e-01;

Matches 8; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

Db 163 LRLLGSRDIRRAS 177

QY 1 LRALLTAPRSLRSS 15

RESULT 13

ENTRY title G70575 #type complete

ORGANISM #formal_name Mycobacterium tuberculosis

DATE 17-Jul-1993 #sequence_revision 17-Jul-1998 #text_change 17-Jul-1998

ACCESSIONS G70575

REFERENCE A70500

#authors Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher,

C.; Harris, D.; Gordon, S.V.; Eigmeier, K.; Gas, S.; Barry III, C.E.; Tekala, F.; Badcock, K.; Basham, D.; Brown, D.; Chillingworth, T.; Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holroyd, S.; Hornsby, T.; Jagels, K.; Krogh, A.; McLean, J.; Moule, S.; Murphy, L.; Oliver, S.; Osborne, J.; Quail, M.A.;

```
Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.;
Skelton, S.; Squares, S.; Squares, R.; Sulston, J.E.;
Taylor, K.; Whitehead, S.; Barrell, B.G.
#journal Nature (1998) 393:537-544
#title Deciphering the biology of Mycobacterium tuberculosis from
the complete genome sequence.
#cross-references MUID:98295987
#accession G70575
##status preliminary: nucleic acid sequence not shown;
translation not shown
##molecule_type DNA
##residues 1-215 #label COL
##cross-references GB:Z95324; GB:AL123456; NID:g3261760; PID:e315475;
PID:g2094839
##experimental_source strain H37Rv
GENETICS
#gene Rv0358
SUMMARY #length 215 #molecular-weight 23102 #checksum 4474
Query Match 60.4%; Score 61; DB 2; Length 215;
Best Local Similarity 53.3%; Pred. No. 4.63e+00;
Matches 8; Conservative 5; Mismatches 2; Indels 0; Gaps 0;
Db 189 LRGVAPRPVRRST 203
|| :|||:||||
QY 1 LRALLTAPRSLRSS 15
RESULT 14
ENTRY S55543 #type complete
reverse transcriptase - fruit fly (Drosophila melanogaster)
#formal_name Drosophila melanogaster
#journal Nature (1998) 393:537-544
#title BS a novel LINE-like element in Drosophila melanogaster.
#cross-references MUID:95273172
#accession S55543
##status preliminary: nucleic acid sequence not shown
##molecule_type DNA
##residues 1-860 #label UDO
##cross-references EMBL:X77571
##note the nucleotide sequence was submitted to the EMBL Data
Library, February 1994
##note the complete translation is not shown
#accession S55544
##status preliminary: translation not shown
##molecule_type DNA
##residues 57-860 #label UD2
##cross-references EMBL:X77571
GENETICS
#gene FlyBase:BS
SUMMARY #length 860 #molecular-weight 98647 #checksum 4270
Query Match 60.4%; Score 61; DB 2; Length 860;
Best Local Similarity 57.1%; Pred. No. 4.63e+00;
Matches 8; Conservative 1; Mismatches 5; Indels 0; Gaps 0;
Db 256 RELTOKRRLRRRA 269
| ||| | |||
QY 2 RALLTAPRSLRSS 15
RESULT 15
ENTRY D64935 #type complete
hypothetical protein b1756 - Escherichia coli (strain K-12)
#formal_name Escherichia coli
#journal Nature (1998) 393:537-544
#title Deciphering the biology of Mycobacterium tuberculosis from
the complete genome sequence.
#cross-references MUID:98295987
#accession G70575
##status preliminary: nucleic acid sequence not shown;
translation not shown
##molecule_type DNA
##residues 1-215 #label COL
##cross-references GB:Z95324; GB:AL123456; NID:g3261760; PID:e315475;
PID:g2094839
##experimental_source strain H37Rv
GENETICS
#gene Rv0358
SUMMARY #length 215 #molecular-weight 23102 #checksum 4474
Query Match 60.4%; Score 61; DB 2; Length 215;
Best Local Similarity 53.3%; Pred. No. 4.63e+00;
Matches 8; Conservative 5; Mismatches 2; Indels 0; Gaps 0;
Db 189 LRGVAPRPVRRST 203
|| :|||:||||
QY 1 LRALLTAPRSLRSS 15
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ACCESSIONS D64935
REFERENCE A64720
#authors Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.;
Burland, V.; Riley, M.; Collado-Vides, J.; Glasner, J.D.;
Rode, C.K.; Mayhew, G.F.; Gregor, J.; Davis, N.W.;
Kirkpatrick, H.A.; Goeden, M.A.; Rose, D.J.; Mau, B.; Shao,
Y.
#journal Science (1997) 277:1453-1462
#title The complete genome sequence of Escherichia coli K-12.
#cross-references MUID:97426617
#accession D64935
##status preliminary: nucleic acid sequence not shown;
translation not shown
##molecule_type DNA
##residues 1-217 #label BLAT
##cross-references GB:AE000270; GB:U000096; NID:g1788045; PID:g1788053;
UMGP:b1756
##experimental_source strain K-12, substrain MG1655
KEYWORDS #superfamily ATP-binding cassette homology
FEATURE P-loop
17-207 #domain ATP-binding cassette homology #label ABC\
34-41 #region nucleotide-binding motif A (P-loop)
SUMMARY #length 217 #molecular-weight 24016 #checksum 7949
Query Match 59.4%; Score 60; DB 2; Length 217;
Best Local Similarity 63.6%; Pred. No. 6.76e+00;
Matches 7; Conservative 3; Mismatches 1; Indels 0; Gaps 0;
Db 145 LRALLAOPKAL 155
| ||| : |||
QY 1 LRALLTAPRSL 11
```

Search completed: Wed Jun 16 13:19:25 1999
Job time : 23 secs.

MSRCH_PP protein - protein database search, using Smith-Waterman algorithm
Run on: Wed Jun 16 13:19:41 1999; MasPar time 2.25 Seconds
Tabular output not generated.
188.112 Million cell updates/sec

Title: >US-09-027-777B-2
Description: (1-15) from US0902777B.pep
Perfect Score: 101
Sequence: 1 LRLALTAPRSLRRSS 15

Scoring table: PAM 150
Gap 15

Searched: 77977 seqs, 28268293 residues

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database: swiss-prot37
1:swissprot

Statistics: Mean 28.009; Variance 37.502; scale 0.747

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	Length	ID	Description	Pred. No.
1	101	100.0	152	1 ANF_BOVIN	ATRIAL NATRIURETIC FAC	2.41e-09
2	101	100.0	153	1 ANF_HUMAN	ATRIAL NATRIURETIC FAC	2.41e-09
3	101	100.0	153	1 ANF_RABIT	ATRIAL NATRIURETIC FAC	2.41e-09
4	98	97.0	149	1 ANF_CANPA	ATRIAL NATRIURETIC FAC	1.25e-08
5	98	97.0	150	1 ANF_PIG	ATRIAL NATRIURETIC FAC	1.25e-08
6	98	97.0	153	1 ANF_HORSE	ATRIAL NATRIURETIC FAC	1.25e-08
7	95	94.1	128	1 ANF_CAVPO	ATRIAL NATRIURETIC FAC	6.41e-08
8	95	94.1	128	1 ANF_MOUSE	ATRIAL NATRIURETIC FAC	6.41e-08
9	95	94.1	122	1 ANF_RAT	ATRIAL NATRIURETIC FAC	6.41e-08
10	88	87.1	145	1 ANF_RANCA	ATRIAL NATRIURETIC FAC	2.68e-06
11	66	65.3	758	1 L2DT_DROME	LETHAL(2)DENTICLELESS	1.38e-01
12	59	58.4	96	1 YFJF_ECOLI	HYPOTHETICAL 10.8 KD P	2.96e+00
13	59	58.4	101	1 YFJF_VIBCH	HYPOTHETICAL 11.6 KD P	2.96e+00
14	59	58.4	102	1 YFJF_HAEIN	HYPOTHETICAL PROTEIN H	2.96e+00
15	59	58.4	236	1 URER_ECOLI	UREASE OPERON TRANSCRIPT	2.96e+00
16	59	58.4	366	1 NOLL_RHISN	MODULATION PROTEIN NOL	2.96e+00
17	59	58.4	529	1 HXA_HUMAN	BETA-HEXOSAMINIDASE AL	2.96e+00
18	59	58.4	649	1 HS70_CHLRE	HEAT SHOCK 70 KD PROTE	2.96e+00
19	58	57.4	341	1 YGLI_SFECO	HYPOTHETICAL PROTEIN I	4.51e+00
20	58	57.4	528	1 HEXA_MOUSE	BETA-HEXOSAMINIDASE AL	4.51e+00
21	58	57.4	655	1 IDUA_CANPA	ALPHA-L-IDURONIDASE PR	4.51e+00
22	57	56.4	335	1 OTCC_PSEAE	ORNITHINE CARBAMOYLTRA	6.82e+00
23	57	56.4	857	1 V2A_CWVNT	PROBABLE RNA-DIRECTED	6.82e+00

24	57	56.4	857	1 V2A_CMVB	PROBABLE RNA-DIRECTED	6.82e+00
25	57	56.4	857	1 V2A_CMVFN	PROBABLE RNA-DIRECTED	6.82e+00
26	57	56.4	857	1 V2A_CMVFI	PROBABLE RNA-DIRECTED	6.82e+00
27	57	56.4	857	1 V2A_CMVY	PROBABLE RNA-DIRECTED	6.82e+00
28	57	56.4	857	1 V2A_CMVMB	PROBABLE RNA-DIRECTED	6.82e+00
29	57	56.4	858	1 V2A_CMVBS	PROBABLE RNA-DIRECTED	6.82e+00
30	57	56.4	858	1 V2A_CMVK	PROBABLE RNA-DIRECTED	6.82e+00
31	57	56.4	1473	1 OVOS_CHICK	OVOSTATIN PRECURSOR (O	6.82e+00
32	57	56.4	2201	1 TENA_HUMAN	TENASCIN PRECURSOR (TN	6.82e+00
33	56	55.4	322	1 HS70_ONCVO	HEAT SHOCK 70 KD PROTE	1.02e+01
34	56	55.4	368	1 RF2_TREPA	PEPTIDE CHAIN RELEASE	1.02e+01
35	56	55.4	373	1 GSPL_XANCP	GENERAL SECRETION PATH	1.02e+01
36	56	55.4	380	1 MODD_AZOVI	MOLYBDENUM TRANSPORT A	1.02e+01
37	56	55.4	640	1 HS7A_CAEEL	HEAT SHOCK 70 KD PROTE	1.02e+01
38	56	55.4	644	1 HS70_BRUMA	HEAT SHOCK 70 KD PROTE	1.02e+01
39	56	55.4	1302	1 BCSC_ACEXY	CELLULOSE SYNTHASE OPE	1.02e+01
40	55	54.5	30	1 ANF_RANRI	ATRIAL NATRIURETIC FAC	1.53e+01
41	55	54.5	506	1 PID6_NECRA	PISATIN DEMETHYLASE (E	1.53e+01
42	55	54.5	744	1 BISC_RHOSH	BIOTIN SULFOXIDE REDUC	1.53e+01
43	55	54.5	865	1 ENV_HVIRH	ENVELOPE POLYPROTEIN G	1.53e+01
44	55	54.5	3587	1 SRF2_BACSU	SURFECTIN SYNTHETASE S	1.53e+01
45	55	54.5	3587	1 SRF1_BACSU	SURFECTIN SYNTHETASE S	1.53e+01

ALIGNMENTS

RESULT	1	STANDARD;	PRT;	152 AA.
ID	ANF_BOVIN			
AC	P07501;			
DT	01-APR-1988 (REL. 07, CREATED)			
DT	01-MAR-1989 (REL. 10, LAST SEQUENCE UPDATE)			
DT	01-OCT-1996 (REL. 34, LAST ANNOTATION UPDATE)			
DE	ATRIAL NATRIURETIC FACTOR PRECURSOR (ANF) (ATRIAL NATRIURETIC PEPTIDE)			
DE	(ANF) (PREPROMATRIODILATIN).			
GN	NPPA.			
OS	BOS TAURUS (BOVINE).			
OC	EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA;			
OC	ARTIODACTYLA; RUMINANTIA; PECORA; BOVOIDEA; BOVIDAE; BOS.			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE; 86215205.			
RA	VLASUK G.P., MILLER J., BENCEN G.H., LEWICKI J.A.;			
RT	"Structure and analysis of the bovine atrial natriuretic peptide precursor gene."			
RL	BIOCHEM. BIOPHYS. RES. COMMUN. 136:396-403(1986).			
RN	[2]			
RP	SEQUENCE OF 123-150.			
RX	MEDLINE; 86173941.			
RA	ONG H., MCNICOLL N., LAZURE C., SEIDAH N., CHRETIEN M., CANTIN M.,			
RT	"Purification and sequence determination of bovine atrial natriuretic factor."			
RL	LIFE SCI. 38:1309-1315(1986).			
CC	!- FUNCTION: ATRIAL NATRIURETIC FACTOR (ANF) IS A POTENT VASOACTIVE			
CC	SUBSTANCE SYNTHESIZED IN MAMMALIAN ATRIA AND IS THOUGHT TO PLAY A			
CC	KEY ROLE IN CARDIOVASCULAR HOMEOSTASIS. HAS A CGMP-STIMULATING			
CC	ACTIVITY.			
CC	!- A DISULFIDE BOND IS REQUIRED FOR FULL ACTIVITY OF ATRIOPEPTINS.			
CC	!- SIMILARITY: BELONGS TO THE NATRIURETIC PEPTIDES FAMILY.			
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DR	EMBL; M13145; G162666;			
DR	PIR; A24247; AWBO.			
DR	PROSITE; PS00363; NATRIURETIC_PEPTIDE; 1.			
DR	PFAM; PF00212; ANP; 1.			
KW	VASOACTIVE; SIGNAL.			

FT SIGNAL 1 24
 FT PEPTIDE 123 150 ATRIAL NATRIURETIC PEPTIDE, ALPHA (ANP).
 FT DISULFID 129 145
 SQ SEQUENCE 152 AA: CF200882 CRC32;
 Query Match 100.0%; Score 101; DB 1; Length 152;
 Best Local Similarity 100.0%; Pred. No. 2.41e-09;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Db 114 LRLLTAPRSLRRSS 128
 1 LRLLTAPRSLRRSS 15
 QY
 RESULT 2
 ID ANF_HUMAN STANDARD; PRT; 153 AA.
 AC P01160;
 DT 21-JUL-1986 (REL. 01, CREATED)
 DT 13-AUG-1987 (REL. 05, LAST SEQUENCE UPDATE)
 DT 15-DEC-1998 (REL. 37, LAST ANNOTATION UPDATE)
 DE ATRIAL NATRIURETIC FACTOR PRECURSOR (ANF) (ATRIAL NATRIURETIC PEPTIDE)
 DE (ANP) (PREPRONATRIODILATIN).
 GN NPFA OR PND.
 GN HOMO SAPIENS (HUMAN).
 OS EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA;
 OC PRIMATES; CATARRHINI; HOMINIDAE; HOMO.
 RN
 RN SEQUENCE OF 1-151 FROM N.A.
 RP MEDLINE: 84219799.
 RX OKAWA S., IMAI M., UENO A., TANAKA S., NOGUCHI T., NAKAZATO H.,
 RA KANGAWA K., FUKUDA A., MATSUO H.;
 RT "Cloning and sequence analysis of cDNA encoding a precursor for human
 RT atrial natriuretic polypeptide.";
 RL NATURE 309:724-726(1984).
 RN
 RN SEQUENCE OF 1-151 FROM N.A.
 RP MEDLINE: 84295577.
 RX NAKAYAMA K., OHKUBO H., HIROSE T., INAYAMA S., NAKANISHI S.;
 RA "mRNA sequence for human cardiodilatin-atrial natriuretic factor
 RT precursor and regulation of precursor mRNA in rat atria.";
 RL NATURE 310:699-701(1984).
 RN
 RN SEQUENCE OF 1-151 FROM N.A.
 RP MEDLINE: 85061626.
 RX NEMER M., CHAMBERLAND M., SIROIS D., ARGENTIN S., DROUIN J.,
 RA DIXON R.A.F., ZIVIN R.A., CONDRA J.H.;
 RT "Gene structure of human cardiac hormone precursor,
 RT pronatriodilatin.";
 RL NATURE 312:654-656(1984).
 RN
 RN SEQUENCE OF 1-151 FROM N.A.
 RP MEDLINE: 85061627.
 RX GREENBERG B.D., BENCEN G.H., SEILHAMER J.J., LEWICKI J.A.,
 RA FIDDES J.C.;
 RT "Nucleotide sequence of the gene encoding human atrial natriuretic
 RT factor precursor.";
 RL NATURE 312:656-658(1984).
 RN
 RN SEQUENCE OF 1-151 FROM N.A.
 RP MEDLINE: 85065766.
 RX SEIDMAN C.E., BLOCH K.D., KLEIN K.A., SMITH J.A., SEIDMAN J.G.;
 RA "Nucleotide sequences of the human and mouse atrial natriuretic
 RT factor genes.";
 RL SCIENCE 226:1206-1209(1984).
 RN
 RN SEQUENCE OF 1-151 FROM N.A.
 RP ERINGTON H.;
 RL SUBMITTED (MAY-1998) TO EMBL/GENBANK/DBJ DATA BANKS.
 RN
 RN SEQUENCE OF 118-153 FROM N.A.
 RP MEDLINE: 85038509.
 RX ZIVIN R.A., CONDRA J.H., DIXON R.A.F., SEIDAH N.G., CHRETIEN M.,
 RA NEMER M., CHAMBERLAND M., DROUIN J.;

RT "Molecular cloning and characterization of DNA sequences encoding rat
 RT and human atrial natriuretic factors.";
 RL PROC. NATL. ACAD. SCI. U.S.A. 81:6325-6329(1984).
 RN
 RN SEQUENCE OF 1-75 FROM N.A.
 RX MEDLINE: 85096983.
 RA MAKI M., PARMENTIER M., INAGAMI T.;
 RT "Cloning of genomic DNA for human atrial natriuretic factor.";
 RL BIOCHEM. BIOPHYS. RES. COMMUN. 123:797-802(1984).
 RN
 RN SEQUENCE OF 124-151.
 RX MEDLINE: 84128019.
 RA KANGAWA K., MATSUO H.;
 RT "Purification and complete amino acid sequence of alpha-human atrial
 RT natriuretic polypeptide (alpha-hANP)."
 RL BIOCHEM. BIOPHYS. RES. COMMUN. 118:131-139(1984).
 RN
 RN STRUCTURE BY NMR OF 124-151 MUTANT SELECTIVE FOR NPR-C RECEPTOR.
 RX MEDLINE: 94318633.
 RA FAIRBROTHER W.J., McDOWELL R.S., CUNNINGHAM B.C.;
 RT "Solution conformation of an atrial natriuretic peptide variant
 RT selective for the type A receptor.";
 RL BIOCHEMISTRY 33:8897-8904(1994).
 CC
 CC !- FUNCTION: ATRIAL NATRIURETIC FACTOR (ANF) IS A POTENT VASOACTIVE
 CC SUBSTANCE SYNTHESIZED IN MAMMALIAN ATRIA AND IS THOUGHT TO PLAY A
 CC KEY ROLE IN CARDIOVASCULAR HOMEOSTASIS. HAS A GMP-STIMULATING
 CC ACTIVITY.
 CC
 CC !- THE HUMAN GENOME CONTAINS 2 DIFFERENT PREPRONATRIODILATIN GENES
 CC ONE CODES FOR 2 ARG RESIDUES AT THE C-TERMINUS THAT ARE CLEAVED
 CC TO FORM THE MATURE PEPTIDE, WHILE THE OTHER ENDS IN A TERMINATION
 CC CODON IMMEDIATELY AFTER THE LAST CODON OF THE MATURE PEPTIDE.
 CC
 CC !- SIMILARITY: BELONGS TO THE NATRIURETIC PEPTIDES FAMILY.
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 CC
 EMBL: X01470; G825625;
 DR EMBL: X02558; G825625; JOINED.
 DR EMBL: K02043; G178630; -.
 DR EMBL: X01471; E27452; ALT_SEQ.
 DR EMBL: K02044; G178632; -.
 DR EMBL: AL021155; E1294859; -.
 DR EMBL: M30262; G180182; -.
 DR EMBL: K02399; G178634; -.
 DR PIR: A01424; ANHU.
 DR PIR: A22693; A22693.
 DR PIR: A32733; A32733.
 DR PDB: 1ANP; 07-APR-95.
 DR MIM: 108780; -.
 DR PROSITE: PS00263; NATRIURETIC_PEPTIDE; 1.
 DR PFAM: PF00212; ANP; 1.
 KW VASOACTIVE; SIGNAL; 3D-STRUCTURE.
 FT SIGNAL 1 25
 FT PEPTIDE 26 55 CARDIODILATIN-RELATED PEPTIDE (CDP).
 FT PEPTIDE 124 151 ATRIAL NATRIURETIC PEPTIDE, ALPHA (ANP).
 FT DISULFID 130 146 BY SIMILARITY.
 FT VARIANT 152 153 MISSING (IN ONE OF THE TWO GENES).
 SQ SEQUENCE 153 AA: C24A68AF CRC32;
 Query Match 100.0%; Score 101; DB 1; Length 153;
 Best Local Similarity 100.0%; Pred. No. 2.41e-09;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Db 115 LRLLTAPRSLRRSS 129
 1 LRLLTAPRSLRRSS 15
 QY

RESULT 3
ID ANF_RABBIT STANDARD: PRT: 153 AA.
AC P07500:
DT 01-APR-1988 (REL. 07, CREATED)
DT 01-APR-1988 (REL. 07, LAST SEQUENCE UPDATE)
DT 01-OCT-1996 (REL. 34, LAST ANNOTATION UPDATE)
DE ATRIAL NATRIURETIC FACTOR PRECURSOR (ANF) (ATRIAL NATRIURETIC PEPTIDE)
DE (ANP) (PREPRONATRIODILATIN).
GN NPFA.
OS ORCTOLAGUS CUNICULUS (RABBIT).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA;
OC LAGOMORPHA; LEPORIDAE; ORICTOLAGUS.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE: 86076957.
RA OIKAWA S., IMAI M., INUZUKA C., TAWARAGI Y., NAKAZATO H., MATSUO H.;
RT "Structure of dog and rabbit precursors of atrial natriuretic
RT polypeptides deduced from nucleotide sequence of cloned cDNA";
RL BIOCHEM. BIOPHYS. RES. COMMUN. 132:892-899(1985).
CC -!- FUNCTION: ATRIAL NATRIURETIC FACTOR (ANF) IS A POTENT VASOACTIVE
CC SUBSTANCE SYNTHESIZED IN MAMMALIAN ATRIA AND IS THOUGHT TO PLAY A
CC KEY ROLE IN CARDIOVASCULAR HOMEOSTASIS. HAS A CGMP-STIMULATING
CC ACTIVITY.
CC -!- A DISULFIDE BOND IS REQUIRED FOR FULL ACTIVITY OF ATRIOPEPTINS.
CC -!- SIMILARITY: BELONGS TO THE NATRIURETIC PEPTIDES FAMILY.
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CC
CC EMBL: M12046; G164771;
CC PIR: B25302; AMRB.
CC PROSITE: PS00263; NATRIURETIC_PEPTIDE: 1.
CC PFAM: PF00212; ANP: 1.
CC VASOACTIVE; SIGNAL. 25
FT SIGNAL 1
FT PEPTIDE 124 151 ATRIAL NATRIURETIC PEPTIDE, ALPHA (ANP).
FT DISULFID 130 146
FT SEQUENCE 153 AA; 16843 MW; 1FA4FB42 CRC32;
Query Match 100.0%; Score 101; DB 1; Length 153;
Best Local Similarity 100.0%; Pred. No. 2.41e-09;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Db 115 LRALLTAPRSLSRSS 129
QY 1 LRALLTAPRSLSRSS 15
|||||
RESULT 4
ID ANF_CANFA STANDARD: PRT: 149 AA.
AC P07499:
DT 01-APR-1988 (REL. 07, CREATED)
DT 01-APR-1988 (REL. 07, LAST SEQUENCE UPDATE)
DT 01-OCT-1996 (REL. 34, LAST ANNOTATION UPDATE)
DE ATRIAL NATRIURETIC FACTOR PRECURSOR (ANF) (ATRIAL NATRIURETIC PEPTIDE)
DE (ANP) (PREPRONATRIODILATIN).
GN NPFA.
OS CANIS FAMILIARIS (DOG).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA;
OC CARNIVORA; FISSIPEDIA; CANIDAE; CANIS.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE: 86076957.
RA OIKAWA S., IMAI M., INUZUKA C., TAWARAGI Y., NAKAZATO H., MATSUO H.;
RT "Structure of dog and rabbit precursors of atrial natriuretic
RT polypeptides deduced from nucleotide sequence of cloned cDNA";
RL BIOCHEM. BIOPHYS. RES. COMMUN. 132:892-899(1985).
CC -!- FUNCTION: ATRIAL NATRIURETIC FACTOR (ANF) IS A POTENT VASOACTIVE

CC SUBSTANCE SYNTHESIZED IN MAMMALIAN ATRIA AND IS THOUGHT TO PLAY A
CC KEY ROLE IN CARDIOVASCULAR HOMEOSTASIS. HAS A CGMP-STIMULATING
CC ACTIVITY.
CC -!- A DISULFIDE BOND IS REQUIRED FOR FULL ACTIVITY OF ATRIOPEPTINS.
CC -!- SIMILARITY: BELONGS TO THE NATRIURETIC PEPTIDES FAMILY.
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CC
CC EMBL: M12045; G163901;
CC PIR: A25302; AWDG.
CC PROSITE: PS00263; NATRIURETIC_PEPTIDE: 1.
CC PFAM: PF00212; ANP: 1.
CC VASOACTIVE; SIGNAL. 23
FT SIGNAL 1
FT PEPTIDE 122 149 ATRIAL NATRIURETIC PEPTIDE, ALPHA (ANP).
FT DISULFID 128 144
FT SEQUENCE 149 AA; 15819 MW; D4F3A6CF CRC32;
Query Match 97.0%; Score 98; DB 1; Length 149;
Best Local Similarity 93.3%; Pred. No. 1.25e-08;
Matches 14; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
Db 113 LRALLTAPRSLSRSS 127
QY 1 LRALLTAPRSLSRSS 15
|||||
RESULT 5
ID ANF_PIG STANDARD: PRT: 150 AA.
AC P24259:
DT 01-MAR-1992 (REL. 21, CREATED)
DT 01-MAR-1992 (REL. 21, LAST SEQUENCE UPDATE)
DT 01-OCT-1996 (REL. 34, LAST ANNOTATION UPDATE)
DE ATRIAL NATRIURETIC FACTOR PRECURSOR (ANF) (ATRIAL NATRIURETIC PEPTIDE)
DE (ANP) (PREPRONATRIODILATIN).
GN NPFA.
OS SUS SCROFA (PIG).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA;
OC ARTIODACTYLA; SUIFORMES; SUINA; SUIDAE; SUS.
RN [1]
RP SEQUENCE FROM N.A.
RX TISSUE-HEART RIGHT ATRIUM;
RX MEDLINE: 91067478.
RA MAEGERT H.J., APPELHANS H., GASSEN H.G., FORSSMANN W.G.;
RT "Nucleotide sequence of a porcine prepro atrial natriuretic peptide
RT (ANP) cDNA";
RL NUCLEIC ACIDS RES. 18:6704-6704(1990).
RN [2]
RP SEQUENCE OF 25-150.
RX TISSUE-HEART RIGHT ATRIUM;
RX MEDLINE: 85124561.
RA FORSSMANN W.G., BIRR C., CARLQUIST M., CHRISTMANN M., FINKE R.,
RA HENSCHEN A., HOCK D., KIRCHHEIM H., KREYE V., LOTTSPRECH F., MEYER J.,
RA MOTT V., REINECKE M.;
RT "The auricular myocardiocytes of the heart constitute an endocrine
RT organ. Characterization of a porcine cardiac peptide hormone,
RT cardiodilatin-126";
RL CELL TISSUE RES. 238:425-430(1984).
CC -!- FUNCTION: ATRIAL NATRIURETIC FACTOR (ANF) IS A POTENT VASOACTIVE
CC SUBSTANCE SYNTHESIZED IN MAMMALIAN ATRIA AND IS THOUGHT TO PLAY A
CC KEY ROLE IN CARDIOVASCULAR HOMEOSTASIS. HAS A CGMP-STIMULATING
CC ACTIVITY.
CC -!- A DISULFIDE BOND IS REQUIRED FOR FULL ACTIVITY OF ATRIOPEPTINS.
CC -!- SIMILARITY: BELONGS TO THE NATRIURETIC PEPTIDES FAMILY.
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CC -----
 CC EMBL: X54669; G1884; -
 DR PIR: S13107; S13107;
 DR PROSITE; PS00263; NATRIURETIC_PEPTIDE; 1.
 DR PFAM; PF00212; ANP; 1.
 CC KW VASOACTIVE; SIGNAL.
 FT SIGNAL 1 24
 FT PEPTIDE 25 54
 FT -----
 FT CARDIODILATIN-RELATED PEPTIDE (CDP)
 FT (BY SIMILARITY).
 FT PEPTIDE 123 150
 FT ATRIAL NATRIURETIC PEPTIDE, ALPHA (ANP).
 FT DISULFID 129 145
 FT BY SIMILARITY.
 SQ SEQUENCE 150 AA; 16351 MW; 4FF67B94 CRC32;

Query Match 97.0%; Score 98; DB 1; Length 150;
 Best Local Similarity 93.3%; Pred. No. 1.25e-08;
 Matches 14; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Db 114 LRALLAPRSLSRSS 128
 QY 1 LRALLTAPRSLSRSS 15
 RESULT 6
 ID ANF_HORSE STANDARD; PRT; 153 AA.
 AC P27104;
 DT 01-AUG-1992 (REL. 23, CREATED)
 DT 01-AUG-1992 (REL. 34, LAST SEQUENCE UPDATE)
 DT 01-OCT-1996 (REL. 34, LAST ANNOTATION UPDATE)
 DE ATRIAL NATRIURETIC FACTOR PRECURSOR (ANP) (ATRIAL NATRIURETIC PEPTIDE)
 DE (ANP) (PREPRONATRIODILATIN).
 GN NPFA.
 OS EQUUS CABALLUS (HORSE).
 OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA;
 CC PERISSODACTYLA; EQUIDAE; EQUUS.
 CC [1]
 CC SEQUENCE FROM N.A.
 RC STRAIN-ADAMITICUS; TISSUE-HEART ATRIUM;
 RA MAEGERT H. J., RICHTER R., SCHMAEDING G., FORSSMANN W. G.;
 RL SUBMITTED (MAR-1991) TO EMBL/GENBANK/DBJ DATA BANKS.
 CC -1- FUNCTION: ATRIAL NATRIURETIC FACTOR (ANP) IS A POTENT VASOACTIVE
 CC SUBSTANCE SYNTHESIZED IN MAMMALIAN ATRIA AND IS THOUGHT TO PLAY A
 CC KEY ROLE IN CARDIOVASCULAR HOMEOSTASIS. HAS A CGMP-STIMULATING
 CC ACTIVITY.
 CC -1- A DISULFIDE BOND IS REQUIRED FOR FULL ACTIVITY OF ATRIOPEPTINS.
 CC -1- SIMILARITY: BELONGS TO THE NATRIURETIC PEPTIDES FAMILY.

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CC EMBL: X58563; G1009; -
 DR PIR: S14873; S14873;
 DR PROSITE; PS00263; NATRIURETIC_PEPTIDE; 1.
 DR PFAM; PF00212; ANP; 1.
 CC KW VASOACTIVE; SIGNAL.
 FT SIGNAL 1 25
 FT PEPTIDE 124 151
 FT ATRIAL NATRIURETIC PEPTIDE, ALPHA (ANP).
 FT DISULFID 130 146
 FT BY SIMILARITY.
 SQ SEQUENCE 153 AA; 16825 MW; FE5D5F4A CRC32;

Query Match 97.0%; Score 98; DB 1; Length 153;
 Best Local Similarity 93.3%; Pred. No. 1.25e-08;
 Matches 14; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Db 115 LRALLAPRSLSRSS 129
 QY 1 LRALLTAPRSLSRSS 15
 RESULT 7
 ID ANF_CAVPO STANDARD; PRT; 128 AA.
 AC P27596;
 DT 01-AUG-1992 (REL. 23, CREATED)
 DT 01-AUG-1992 (REL. 34, LAST SEQUENCE UPDATE)
 DT 01-OCT-1996 (REL. 34, LAST ANNOTATION UPDATE)
 DE ATRIAL NATRIURETIC FACTOR PRECURSOR (ANP) (ATRIAL NATRIURETIC PEPTIDE)
 DE (ANP) (PREPRONATRIODILATIN) (FRAGMENT).
 GN NPFA.
 OS CAVIA PORCELLUS (GUINEA PIG).
 OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA;
 CC RODENTIA; HYSTRICOGNATHI; CAVIIDAE; CAVIA.
 CC [1]
 CC SEQUENCE FROM N.A.
 RC TISSUE-HEART ATRIUM;
 RA MAEGERT H. J., HANKE M., SCHMEDING G., TEUTEBERG K.,
 RA SCHULZ-KNAPPE P., FORSSMANN W. G.;
 RL SUBMITTED (MAR-1991) TO EMBL/GENBANK/DBJ DATA BANKS.
 CC -1- FUNCTION: ATRIAL NATRIURETIC FACTOR (ANP) IS A POTENT VASOACTIVE
 CC SUBSTANCE SYNTHESIZED IN MAMMALIAN ATRIA AND IS THOUGHT TO PLAY A
 CC KEY ROLE IN CARDIOVASCULAR HOMEOSTASIS. HAS A CGMP-STIMULATING
 CC ACTIVITY.
 CC -1- DEVELOPMENTAL STAGE: ADULT.
 CC -1- A DISULFIDE BOND IS REQUIRED FOR FULL ACTIVITY OF ATRIOPEPTINS.
 CC -1- SIMILARITY: BELONGS TO THE NATRIURETIC PEPTIDES FAMILY.

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CC EMBL: X58562; G49544; -
 DR PIR: S14872; S14872;
 DR PROSITE; PS00263; NATRIURETIC_PEPTIDE; 1.
 DR PFAM; PF00212; ANP; 1.
 CC KW VASOACTIVE.
 FT NON_TER 1 1
 FT PEPTIDE 1 30
 FT CARDIODILATIN-RELATED PEPTIDE (CDP).
 FT DISULFID 99 126
 FT ATRIAL NATRIURETIC PEPTIDE, ALPHA (ANP).
 FT BY SIMILARITY.
 SQ SEQUENCE 128 AA; 13966 MW; 2C2F552D CRC32;

Query Match 94.1%; Score 95; DB 1; Length 128;
 Best Local Similarity 93.3%; Pred. No. 6.41e-08;
 Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Db 90 LRALLDAPRSLSRSS 104
 QY 1 LRALLTAPRSLSRSS 15
 RESULT 8
 ID ANF_MOUSE STANDARD; PRT; 152 AA.
 AC P05125;
 DT 13-AUG-1987 (REL. 05, CREATED)
 DT 13-AUG-1987 (REL. 05, LAST SEQUENCE UPDATE)
 DT 01-OCT-1996 (REL. 34, LAST ANNOTATION UPDATE)
 DE ATRIAL NATRIURETIC FACTOR PRECURSOR (ANP) (ATRIAL NATRIURETIC PEPTIDE)
 DE (ANP) (PREPRONATRIODILATIN).
 GN NPFA OR PND.
 OS MUS MUSCULUS (MOUSE).
 OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA;
 CC RODENTIA; SCIUROGNATHI; MURIDAE; MURINAE; MUS.
 CC [1]
 CC SEQUENCE FROM N.A.

RX MEDLINE; 85065766.
RA SEIDMAN C.E., BLOCH K.D., KLEIN K.A., SMITH J.A., SEIDMAN J.G.;
RT "Nucleotide sequences of the human and mouse atrial natriuretic
RL factor genes";
CC SCIENCE 226:1206-1209(1984).
CC -!- FUNCTION: ATRIAL NATRIURETIC FACTOR (ANF) IS A POTENT VASOACTIVE
CC SUBSTANCE SYNTHESIZED IN MAMMALIAN ATRIA AND IS THOUGHT TO PLAY A
CC KEY ROLE IN CARDIOVASCULAR HOMEOSTASIS. HAS A CGMP-STIMULATING
CC ACTIVITY.
CC -!- A DISULFIDE BOND IS REQUIRED FOR FULL ACTIVITY OF ATRIOPEPTINS.
CC -!- SIMILARITY: BELONGS TO THE NATRIURETIC PEPTIDES FAMILY.
CC
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CC
DR EMBL; K02781; G387099;
DR PIR; A29370; AWMS.
DR MGI; 97367; NPFA.
DR PROSITE; PS00263; NATRIURETIC-PEPTIDE; 1.
DR PFAM; PF00212; ANP; 1.
KW VASOACTIVE; SIGNAL.
FT SIGNAL 1 24
FT PEPTIDE 126 149 AURICULIN A (BY SIMILARITY).
FT PEPTIDE 126 150 AURICULIN B (BY SIMILARITY).
FT PEPTIDE 127 149 ATRIOPEPTIN I (BY SIMILARITY).
FT PEPTIDE 127 147 ATRIOPEPTIN II (BY SIMILARITY).
FT DISULFID 129 145 BY SIMILARITY.
SQ SEQUENCE 152 AA; 16645 MW; 5163CB23 CRC32;

Query Match 94.1%; Score 95; DB 1; Length 152;
Best Local Similarity 86.7%; Pred. NO. 6.41e-08;
Matches 13; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Db 114 LRALLAGPRSLRSS 128
QY 1 LRALLTAPSLRSS 15
IIIIII:IIIIIIII

RESULT 9
ID ANF_RAT STANDARD; PRT; 152 AA.
AC P01161;
DT 21-JUL-1986 (REL. 01, CREATED)
DT 21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)
DT 15-DEC-1998 (REL. 37, LAST ANNOTATION UPDATE)
DE ATRIAL NATRIURETIC FACTOR PRECURSOR (ANF) (ATRIAL NATRIURETIC PEPTIDE)
DE (ANF) (PREPRONATRIODILATIN) [CONTAINS: AURICULINS; ATRIOPEPTINS].
GN NPFA.
OS RATTUS NORVEGICUS (RAT).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA;
OC RODENTIA; SCIUROGNATHI; MURIDAE; MURINAE; RATTUS.
RN [1]
RP SEQUENCE FROM N.A.
RX YAMANAKA M., GREENBERG B., JOHNSON L., SEILHAMER J.J., BREWER M.,
RA FRIEDEMANN T., MILLER J., ATLAS S.A., LARAGH J., LEWICKI J.,
RA FIDDES J.C.;
RT "Cloning and sequence analysis of the cDNA for the rat atrial
RL natriuretic factor precursor.";
RL NATURE 309:719-722(1984).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE; 84219798.
RA YAMANAKA M., GREENBERG B., JOHNSON L., SEILHAMER J.J., BREWER M.,
RA FRIEDEMANN T., MILLER J., ATLAS S.A., LARAGH J., LEWICKI J.,
RA FIDDES J.C.;
RT "Cloning and sequence analysis of the cDNA for the rat atrial
RL natriuretic factor precursor.";
RL NATURE 309:719-722(1984).
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE; 84219798.
RA YAMANAKA M., GREENBERG B., JOHNSON L., SEILHAMER J.J., BREWER M.,
RA FRIEDEMANN T., MILLER J., ATLAS S.A., LARAGH J., LEWICKI J.,
RA FIDDES J.C.;
RT "Cloning and sequence analysis of the cDNA for the rat atrial
RL natriuretic factor precursor.";
RL NATURE 309:719-722(1984).
RN [3]

RP SEQUENCE FROM N.A.
RX MEDLINE; 84256178.
RA SEIDMAN C.E., DUBY A.D., CHOI E., GRAHAM R.M., HABER E., HOWCY C.,
RA SMITH J.A., SEIDMAN J.G.;
RT "The structure of rat preproatrial natriuretic factor as defined by a
RL complementary DNA clone.";
RL SCIENCE 225:324-326(1984).
RN [4]
RP SEQUENCE FROM N.A.
RX MEDLINE; 85061500.
RA KANAKA K., TAWARAGI Y., OIKAWA S., MIZUNO A., SAKURAGAWA Y.,
RA NAKAZATO H., FUKUDA A., MINAMINO N., MATSUO H.;
RT "Identification of rat gamma atrial natriuretic polypeptide and
RL characterization of the cDNA encoding its precursor.";
RL NATURE 312:152-155(1984).
RN [5]
RP SEQUENCE FROM N.A.
RX MEDLINE; 85182558.
RA ARGENTIN S., NEMER M., DROUIN J., SCOTT G.K., KENNEDY B.P.,
RA DAVIES P.L.;
RT "The gene for rat atrial natriuretic factor.";
RL J. BIOL. CHEM. 260:4568-4571(1985).
RN [6]
RP SEQUENCE FROM N.A.
RX MEDLINE; 85038509.
RA ZIVIN R.A., CONDRA J.H., DIXON R.A.F., SEIDAH N.G., CHRETEN M.,
RA NEMER M., CHAMBERLAND M., DROUIN J.;
RT "Molecular cloning and characterization of DNA sequences encoding rat
RL and human atrial natriuretic factors.";
RL PROC. NATL. ACAD. SCI. U.S.A. 81:6325-6329(1984).
RN [7]
RP SEQUENCE FROM N.A.
RX MEDLINE; 88109092.
RA FLYNN T.G.;
RT "The elucidation of the structure of atrial natriuretic factor, a new
RL peptide hormone.";
RL CAN. J. PHYSIOL. PHARMACOL. 65:2013-2020(1987).
RN [8]
RP SEQUENCE OF 38-152 FROM N.A.
RX MEDLINE; 87175636.
RA GARDNER D.G., VLASUK G.P., BAXTER J.D., FIDDES J.C., LEWICKI J.A.;
RT "Identification of atrial natriuretic factor gene transcripts in the
RL central nervous system of the rat.";
RL PROC. NATL. ACAD. SCI. U.S.A. 84:2175-2179(1987).
RN [9]
RP AURICULINS, SEQUENCE, AND SYNTHESIS OF 126-149.
RX MEDLINE; 84219796.
RA ATLAS S.A., KLEINERT H.D., CAMARGO M.J., JANUSZEWICZ A., SEALEY J.E.,
RA LARAGH J.H., SCHILLING J.W., LEWICKI J.A., JOHNSON L.K., MAACK T.;
RT "Purification, sequencing and synthesis of natriuretic and vasoactive
RL rat atrial peptide.";
RL NATURE 309:717-719(1984).
RN [10]
RP SEQUENCE OF 127-149, AND SYNTHESIS.
RX MEDLINE; 84097513.
RA CURRIE M.G., GELLER D.M., COLE B.R., SIEGEL N.R., FOK K.F.,
RA ADAMS S.P., EUBANKS S.R., GALLUPPI G.R., NEEDLEMAN P.;
RT "Purification and sequence analysis of bioactive atrial peptides
RL (atriopeptins).";
RL SCIENCE 223:67-69(1984).
RN [11]
RP SEQUENCE OF 113-150.
RX MEDLINE; 84194062.
RA SEIDAH N.G., LAZURE C., CHRETEN M., THIBAUT G., GARCIA R.,
RA COLTON M., GENEST J., NUTT R.F., BRADY S.F., LYLE T.A., PALEVEDA W.J.,
RA COLTON C.D., CICCAREONE T.M., VEBER D.F.;
RT "Amino acid sequence of homologous rat atrial peptides: natriuretic
RL activity of native and synthetic forms.";
RL PROC. NATL. ACAD. SCI. U.S.A. 81:2640-2644(1984).
RN [12]
RP SEQUENCE OF 25-38.
RX MEDLINE; 88203350.
RA THIBAUT G., MURTHY K.K., GUTKOWSKA J., SEIDAH N.G., LAZURE C.,

RA CHRETIEN M., CANTIN M.;
 RT "NH2-terminal fragment of rat pro-atrial natriuretic factor in the
 RL peptides 9:47-53(1988).
 CC -1- FUNCTION: ATRIAL NATRIURETIC FACTOR (ANF) IS A POTENT VASOACTIVE
 CC SUBSTANCE SYNTHESIZED IN MAMMALIAN ATRIA AND IS THOUGHT TO PLAY A
 CC KEY ROLE IN CARDIOVASCULAR HOMEOSTASIS. HAS A CGMP-STIMULATING
 CC ACTIVITY.
 CC -1- A DISULFIDE BOND IS REQUIRED FOR FULL ACTIVITY OF ATRIOPEPTINS.
 CC -1- SIMILARITY: BELONGS TO THE NATRIURETIC PEPTIDES FAMILY.
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 CC EMBL: M15868; G202904;
 CC EMBL: X00665; G55712;
 CC EMBL: K02062; G202900;
 CC EMBL: X01118; G55717;
 CC EMBL: M27498; G202906;
 CC PIR: A22570; AWRP
 CC PIR: A44190; A44190.
 CC PROSITE: PS00263; NATRIURETIC_PEPTIDE; 1.
 CC PFAM: PF00212; ANP; 1.
 CC KW VASOACTIVE; SIGNAL.
 CC SIGNAL 1 24
 CC PEPTIDE 126 149 AURICULIN A.
 CC PEPTIDE 126 150 AURICULIN B.
 CC PEPTIDE 127 147 ATRIOPEPTIN I.
 CC PEPTIDE 127 149 ATRIOPEPTIN II.
 CC PEPTIDE 127 150 ATRIOPEPTIN III.
 CC DISULFID 129 145
 CC SEQUENCE 152 AA; 16556 MW; 20424875 CRC32;
 Query Match 94.1%; Score 95; DB 1; Length 152;
 Best Local Similarity 86.7%; Pred. No. 6.41e-08;
 Matches 13; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
 Db 114 LRALLAGPRSLRRSS 128
 QY 1 LRALLTAPRSLRRSS 15
 RESULT 10 STANDARD; PRT; 145 AA.
 ID ANF_RANCA
 AC P18909;
 DT 01-NOV-1990 (REL. 16, CREATED)
 DT 01-MAR-1992 (REL. 21, LAST SEQUENCE UPDATE)
 DT 01-FEB-1995 (REL. 31, LAST ANNOTATION UPDATE)
 DE ATRIAL NATRIURETIC FACTOR PRECURSOR (ANF) (ATRIAL NATRIURETIC PEPTIDE)
 DE (ANP).
 OS RANA CATESBETANA (BULL FROG).
 OC EURKYOTA; METAZOA; CHORDATA; VERTEBRATA; AMPHIBIA; BATRACHIA; ANURA;
 OC NEOBATRACHIA; RANOIDEA; RANIDAE; RANINAE; RANA.
 CC
 CC SEQUENCE FROM N.A.
 RA KOJIMA M.;
 RL SUBMITTED (XX-1992) TO EMBL/GENBANK/DDBJ DATA BANKS.
 RN SEQUENCE OF 122-145.
 RC TISSUE=HEART;
 RX MEDLINE: 89025806.
 RA SAKATA J., KANGAWA K., MATSUO H.;
 RT Identification of new atrial natriuretic peptides in frog heart.;
 RL BIOCHEM. BIOPHYS. RES. COMMUN. 155:1338-1345(1988).
 CC -1- FUNCTION: VASOACTIVE ACTIVITY. HAS A CGMP-STIMULATING ACTIVITY.
 CC -1- SIMILARITY: BELONGS TO THE NATRIURETIC PEPTIDES FAMILY.
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 CC EMBL: D01043; D1001314;
 CC PIR: A31510; A31510.
 CC PIR: JQ0947; JQ0947.
 CC PROSITE: PS00263; NATRIURETIC_PEPTIDE; 1.
 CC PFAM: PF00212; ANP; 1.
 CC KW VASOACTIVE; SIGNAL. 23 POTENTIAL.
 CC SIGNAL 1 122 145 ATRIAL NATRIURETIC FACTOR.
 CC PEPTIDE 122 145
 CC DISULFID 125 141
 CC SEQUENCE 145 AA; 15934 MW; 6A1FA352 CRC32;
 Query Match 87.1%; Score 88; DB 1; Length 145;
 Best Local Similarity 80.0%; Pred. No. 2.68e-06;
 Matches 12; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
 Db 109 LRLLNAPRSMRRSS 123
 QY 1 LRALLTAPRSLRRSS 15
 RESULT 11 STANDARD; PRT; 758 AA.
 ID L2DT_DROME
 AC Q24371;
 DT 15-JUL-1998 (REL. 36, CREATED)
 DT 15-JUL-1998 (REL. 36, LAST SEQUENCE UPDATE)
 DT 15-JUL-1998 (REL. 36, LAST ANNOTATION UPDATE)
 DE LETHAL(2)DENTICLELESS PROTEIN (DTL83 PROTEIN).
 GN L(2)DTL OR DTL83.
 OS DROSOPHILA MELANOGASTER (FRUIT FLY).
 OC EURKYOTA; METAZOA; ARTHROPODA; TRACHEATA; HEXAPODA; INSECTA;
 OC PTERYOTA; DIPTERA; BRACHYCERA; MUSCOMORPHA; EPHYDROIDEA;
 CC DROSOPHILIDAE; DROSOPHILA.
 CC
 CC SEQUENCE FROM N.A.
 RC STRAIN=OREGON-R;
 RX MEDLINE: 96257214.
 RA KURZIR-DUMKE U., NEUBAUER M., DEBES A.;
 RT Identification of a novel Drosophila melanogaster heat-shock gene,
 RT lethal(2)denticleless [l(2)dtl], coding for an 83-kDa protein.;
 RL GENE 171:163-170(1996).
 CC -1- SUBCELLULAR LOCATION: CYTOPLASMIC (POTENTIAL).
 CC -1- TISSUE SPECIFICITY: UBQUITOUSLY EXPRESSED DURING EMBRYOGENESIS
 CC WITH NO SIGN OF TISSUE SPECIFICITY IN EXPRESSION UP TO STAGE 17.
 CC -1- DEVELOPMENTAL STAGE: DETECTED AT ALL DEVELOPMENTAL STAGES. THE
 CC EXTREMELY HIGH LEVEL OF TRANSCRIPTION DETECTED IN THE EARLY EMBRYO
 CC AND IN ADULTS IS CAUSED BY MATERNAL MESSAGE.
 CC -1- INDUCTION: BY HEAT SHOCK.
 CC -1- SIMILARITY: CONTAINS 6 WD REPEATS (TRP-ASP DOMAINS).
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 CC
 CC EMBL: X83414; G603539;
 CC FLYBASE; FBgn0013548; l(2)dtl.
 CC PROSITE: PS00678; WD_REPEATS; 1.
 CC PFAM: PF00400; G-beta; 4.
 CC KW HEAT SHOCK; REPEAT; WD REPEAT.
 CC REPEAT 88 118 WD1.
 CC REPEAT 132 163 WD2.
 CC REPEAT 183 238 WD3.
 CC REPEAT 253 292 WD4.

FT REPEAT 309 338 WD5.
 FT REPEAT 351 382 WD6.
 FT DOMAIN 558 567 POLY-ALA.
 FT DOMAIN 672 675 POLY-GLY.
 FT DOMAIN 721 724 POLY-THR.
 SQ SEQUENCE 758 AA; 82352 MW; 8F37E148 CRC32;

Query Match 65.3%; Score 66; DB 1; Length 758;
 Best Local Similarity 61.5%; Pred. No. 1.38e-01;
 Matches 8; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

DB 425 LRLESTPSLRK 437
 QY 1 LRALLTAPSLRR 13

RESULT 12
 ID YFJF_ECOLI STANDARD; PRT; 96 AA.
 AC P52119; P76603;
 DT 01-OCT-1996 (REL. 34, CREATED)
 DT 01-OCT-1996 (REL. 34, LAST SEQUENCE UPDATE)
 DT 01-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE)
 DE HYPOTHETICAL 10.8 KD PROTEIN IN SMPA-SMPB INTERGENIC REGION (F102).
 GN YFJF.
 OS ESCHERICHIA COLI.
 OC BACTERIA; PROTEOBACTERIA; GAMMA SUBDIVISION; ENTEROBACTERIACEAE;
 CC ESCHERICHIA.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-K12 / MG1655;
 RX MEDLINE; 97426617.
 RA BLATTNER F.R., PLUNKETT G. III, BLOCH C.A., PERNA N.T., BURLAND V.,
 RA RILEY M., COLLADO-VIDES J., GLASNER F.D., ROSE C.K., MAYHEW G.F.,
 RA GREGOR J., DAVIS N.W., KIRKPATRICK H.A., GOEDEN M.A., ROSE D.J.,
 RA MAU B., SHAO Y.;
 RL "The complete genome sequence of Escherichia coli K-12.";
 RT SCIENCE 277:1453-1474(1997).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN-K12;
 RA ALBA H., BABA T., FUJITA K., HAYASHI K., HONJO A., HORTUCHI T.,
 RA IKEMOTO K., INADA T., ISONO K., ISONO S., ITOH T., KANAI K.,
 RA KASAI H., KASHIMOTO K., KIM S., KIMURA S., KITAGAWA M.,
 RA KITAKAWA M., MAKINO K., MASUDA S., MIKI T., MIZOBUCHI K., MORI H.,
 RA MOTOMURA K., NAKAMURA Y., NASHIMOTO H., NISHIO Y., OSHIMA T.,
 RA SAITO N., SAMPEI G., SEKI Y., TAGAMI H., TAKEMOTO K., WADA C.,
 RA YAMAMOTO Y., YANO M.;
 RL SUBMITTED (JAN-1997) TO EMBL/GENBANK/DBJ DATA BANKS.
 RN [3]

SEQUENCE OF 1-20 FROM N.A.
 STRAIN-K12;
 MEDLINE; 95023883.
 RA KOMINE Y., KITABATAKE M., YOKOGAWA T., NISHIKAWA K., INOKUCHI H.;
 RT "A tRNA-like structure is present in 10Sa RNA, a small stable RNA
 from Escherichia coli.";
 RL PROC. NATL. ACAD. SCI. U.S.A. 91:9223-9227(1994).
 CC -1- SIMILARITY: STRONG, TO H. INFLUENZAE HI0395.
 CC -----
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 CC -----
 CC EMBL; U36840; G1033114; ALT_INIT.
 DR EMBL; AE000347; G1788971; ALT_INIT.
 DR EMBL; D90888; G1800023;
 DR EMBL; D12501; -; NOT_ANNOTATED_CDS.
 KW HYPOTHETICAL PROTEIN.
 SQ SEQUENCE 96 AA; 10789 MW; F8707FB4 CRC32;

Query Match 58.4%; Score 59; DB 1; Length 96;
 Best Local Similarity 50.0%; Pred. No. 2.96e-00;
 Matches 6; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

DB 76 RPLIADPKELRR 87
 QY 2 RALLTAPSLRR 13

RESULT 13
 ID YFJF_VIBCH STANDARD; PRT; 101 AA.
 AC P52120;
 DT 01-OCT-1996 (REL. 34, CREATED)
 DT 01-OCT-1996 (REL. 34, LAST SEQUENCE UPDATE)
 DT 01-OCT-1996 (REL. 34, LAST ANNOTATION UPDATE)
 DE HYPOTHETICAL 11.6 KD PROTEIN IN SMPA-SMPB INTERGENIC REGION (ORF101).
 OS VIBRIO CHOLERAE.
 OC BACTERIA; PROTEOBACTERIA; GAMMA SUBDIVISION; VIBRIONACEAE; VIBRIO.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-OGAWA 395;
 RC KOVACH M.E., HUGHES K.J., HARKEY C.W., EVERISS K.D., SHAFFER M.D.,
 RA PETERSON K.M.;
 RA SUBMITTED (OCT-1995) TO EMBL/GENBANK/DBJ DATA BANKS.
 CC -1- SIMILARITY: STRONG, TO E. COLI YFJF.
 CC -----
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 CC -----
 CC EMBL; U39088; G1100886;
 DR HYPOTHETICAL PROTEIN.
 KW HYPOTHETICAL PROTEIN.
 SQ SEQUENCE 101 AA; 11613 MW; 104426EF CRC32;

Query Match 58.4%; Score 59; DB 1; Length 101;
 Best Local Similarity 50.0%; Pred. No. 2.96e-00;
 Matches 6; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

DB 77 RPLIADPKELRR 88
 QY 2 RALLTAPSLRR 13

RESULT 14
 ID YFJF_HAEIN STANDARD; PRT; 102 AA.
 AC P43994;
 DT 01-NOV-1995 (REL. 32, CREATED)
 DT 01-NOV-1995 (REL. 32, LAST SEQUENCE UPDATE)
 DT 01-OCT-1996 (REL. 34, LAST ANNOTATION UPDATE)
 DE HYPOTHETICAL PROTEIN HI0395.
 GN HI0395.
 OS HAEMOPHILUS INFLUENZAE.
 OC BACTERIA; PROTEOBACTERIA; GAMMA SUBDIVISION; PASTEURELLACEAE;
 CC HAEMOPHILUS.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-RD / KW20;
 RX MEDLINE; 95350630.
 RA FLEISCHMANN R.D., ADAMS M.D., WHITE O., CLAYTON R.A., KIRKNESS E.F.,
 RA KERLAVAGE A.R., BOLT C.J., TOMB J.-F., DOUGHERTY B.A., MERRICK J.M.,
 RA MCKENNEY K., SUTTON G., FITZHUGH W., FIELDS C.A., GOCAYNE J.D.,
 RA SCOTT J.D., SHIRLEY R., LIU L.-I., GLODER A., KELLEY J.M.,
 RA WEIDMAN J.F., PHILLIPS C.A., SPRIGGS T., HEDBLUM E., COTTON M.D.,
 RA UTTERBACK T.R., HANNA M.C., NGUYEN D.T., SAUDEK D.M., BRANDON R.C.,
 RA FINE L.D., FRITZMAN J.L., FUHRMANN J.L., GEOGHAGEN N.S.M.,
 RA GNEHM C.L., McDONALD L.A., SMALL K.V., FRASER C.M., SMITH H.O.,
 RA VENTER J.C.;
 RT "Whole-genome random sequencing and assembly of Haemophilus
 influenzae Rd.";

RL SCIENCE 269:496-512(1995).
CC -!- SIMILARITY: STRONG, TO E.COLI YFJF.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: U32723; G1573377; -
DR TIGR: H10395; -
KW HYPOTHETICAL PROTEIN.
SQ SEQUENCE 102 AA; 11584 MW; 1B2632C6 CRC32;
Query Match 58.4%; Score 59; DB 1; Length 102;
Best Local Similarity 50.0%; Pred. No. 2.96e+00;
Matches 6; Conservative 4; Mismatches 2; Indels 0; Gaps 0;
Db 75 RPLADPKREIR 86
Y 2 RALLTAPRSLRR 13
RESULT 15
ID URER_ECOLI STANDARD: PRT; 296 AA.
AC P32326;
DT 01-OCT-1993 (REL. 27, CREATED)
DT 01-OCT-1993 (REL. 27, LAST SEQUENCE UPDATE)
DT 01-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE)
DE URASE OPERON TRANSCRIPTIONAL ACTIVATOR.
GN URER.
OS ESCHERICHIA COLI.
OG PLASMID.
OC BACTERIA; PROTEOBACTERIA; GAMMA SUBDIVISION; ENTEROBACTERIACEAE;
OC ESCHERICHIA.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE; 93273714.
RA D'ORAZIO S.E.F., COLLINS C.M.;
RT "The plasmid-encoded urease gene cluster of the family
RT Enterobacteriaceae is positively regulated by UreR, a member of the
RT Arac family of transcriptional activators.";
RL J. BACTERIOL. 175:3459-3467(1993).
CC -!- FUNCTION: POSITIVE REGULATOR OF THE EXPRESSION OF THE UREASE
CC OPERON.
CC -!- SIMILARITY: BELONGS TO THE ARAC/XYLS FAMILY OF TRANSCRIPTIONAL
CC REGULATORS.
CC -----
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CC -----
DR EMBL: L12007; G148159; -
DR PIR: A40593;
DR PROSITE: PS00041; HTH_ARAC_FAMILY_1; 1.
DR PROSITE: PS01124; HTH_ARAC_FAMILY_2; 1.
DR PFAM: PF00165; HTH_2; 1.
KW TRANSCRIPTION REGULATION; DNA-BINDING; ACTIVATOR; PLASMID.
FT DNA_BIND 187 206 H-T-H MOTIF (BY SIMILARITY).
SQ SEQUENCE 296 AA; 34032 MW; B99B27B6 CRC32;
Query Match 58.4%; Score 59; DB 1; Length 296;
Best Local Similarity 58.3%; Pred. No. 2.96e+00;
Matches 7; Conservative 4; Mismatches 1; Indels 0; Gaps 0;
Db 192 KALFTTPSTLRR 203
Y 2 RALLTAPRSLRR 13

OY 2 RALLTAPRSLRR 13

Search completed: Wed Jun 16 13:19:48 1999
Job time : 7 secs.

M P S R E L H

(TM)

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MPsrch_pp protein - protein database search, using Smith-Waterman algorithm
Run on: Wed Jun 16 13:20:04 1999; MasPar time 4.58 Seconds
Tabular output not generated. 178.668 Million cell updates/sec

Title: >US-09-027-777B-2
Description: (1-15) from US09027777B.pep
Perfect Score: 101
Sequence: 1 LRALLTAPRSLRRSS 15

Scoring table: PAM 150
Gap 15

Searched: 179066 seqs, 54579741 residues

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database: sptrembl9
1:sp_archaea 2:sp_bacteria 3:sp_fungi 4:sp_human
5:sp_invertebrate 6:sp_mammal 7:sp_mhc 8:sp_organelle
9:sp_phase 10:sp_plant 11:sp_rodent 12:sp_unclassified
13:sp_vertebrate 14:sp_virus

Statistics: Mean 26.978; Variance 38.734; scale 0.697

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description	Pred. No.
1	101	100.0	151	4 Q13766	ATRIAL NATRIURETIC FAC	1.40e-08
2	101	100.0	151	6 Q46540	ATRIAL NATRIURETIC PEP	1.40e-08
3	94	93.1	155	6 Q29130	CARDIODILATIN, ATRIAL	5.26e-07
4	65	64.4	196	1 Q27778	CYTOCHROME C-TYPE BIOG	5.20e-01
5	63	62.4	1218	5 Q77443	VALYL TRNA SYNTHETASE	1.22e+00
6	61	60.4	215	2 Q05308	HYPOTHETICAL 23.1 KD P	2.83e+00
7	61	60.4	216	12 P97981	70-KDA HEAT SHOCK PROT	2.83e+00
8	61	60.4	373	2 Q33426	GLUCOSYLTRANSFERASE I	2.83e+00
9	60	59.4	246	2 P76909	INNER MEMBRANE PROTEIN	4.28e+00
10	60	59.4	303	2 Q52554	KINASE	4.28e+00
11	60	59.4	642	14 Q68404	ORF UL150.	4.28e+00
12	59	58.4	227	5 Q61790	R12E2.11 PROTEIN.	6.44e+00
13	59	58.4	348	10 Q96517	MAP KINASE KINASE ALPH	6.44e+00
14	59	58.4	348	10 Q80398	MAP KINASE KINASE 5.	6.44e+00
15	59	58.4	514	4 Q75434	ANGIOTENSIN/VASOPRESSI	6.44e+00
16	59	58.4	856	14 Q73295	ENVELOPE GLYCOPROTEIN.	6.44e+00
17	59	58.4	856	14 Q73299	ENVELOPE GLYCOPROTEIN.	6.44e+00
18	59	58.4	109519	11 Q60519	SEMAPHORIN G PRECURSOR	6.44e+00
19	58	57.4	366	10 Q80397	MAP KINASE KINASE 4.	9.64e+00
20	58	57.4	461	5 Q21004	F58G6.1 PROTEIN.	9.64e+00

21	58	57.4	528	11 Q64246	HEXOSAMINIDASE A (BETA	9.64e+00
22	58	57.4	587	2 Q53609	SALI MODIFICATION METH	9.64e+00
23	58	57.4	856	14 Q73296	ENVELOPE GLYCOPROTEIN.	9.64e+00
24	58	57.4	1171	2 Q69825	PEPTIDE SYNTHASE.	9.64e+00
25	57	56.4	43	2 Q43889	PLASMD PIP501 COPR, R	1.44e+01
26	57	56.4	238	2 Q53167	LCRABDE GENES, COMPLE	1.44e+01
27	57	56.4	339	2 P72171	ORUR.	1.44e+01
28	57	56.4	493	2 Q06294	HYPOTHETICAL 53.0 KD P	1.44e+01
29	57	56.4	857	14 Q83261	2A. PROTEIN.	1.44e+01
30	57	56.4	858	14 Q66144	CMV-SD 2A.	1.44e+01
31	57	56.4	878	10 Q04624	SIMILARITY TO MEMBRANE	1.44e+01
32	57	56.4	1104	2 Q51934	REVERSE GYRASE.	1.44e+01
33	57	56.4	1551	4 Q14160	KIAA0147 PROTEIN (FRAG	1.44e+01
34	57	56.4	2019	11 Q64706	TENASCIN C PRECURSOR.	1.44e+01
35	57	56.4	2873	14 Q93075	POLYPROTEIN.	1.44e+01
36	56	55.4	41	2 Q54154	PLASMD PAM-BETAL ADEN	2.13e+01
37	56	55.4	43	2 Q03620	HYPOTHETICAL 4.8 KD PR	2.13e+01
38	56	55.4	43	2 P72470	HYPOTHETICAL 4.8 KD PR	2.13e+01
39	56	55.4	242	2 Q85883	HYPOTHETICAL 25.8 KD P	2.13e+01
40	56	55.4	640	5 Q93601	HSP-1 PROTEIN.	2.13e+01
41	56	55.4	677	3 Q14331	HYPOTHETICAL 74.2 KD P	2.13e+01
42	56	55.4	709	2 Q52772	POTATIVE ABC TRANSPORT	2.13e+01
43	56	55.4	864	14 Q70000	ENVELOPE GLYCOPROTEIN	2.13e+01
44	56	55.4	1746	6 Q29116	TENASCIN PRECURSOR (TN	2.13e+01
45	55	54.5	3052	14 Q82933	JOHNSON GRASS MOSAIC V	3.15e+01

ALIGNMENTS

RESULT 1	PRELIMINARY;	PRT;	151 AA.
ID Q13766	01-NOV-1996 (TREMREL. 01, CREATED)		
AC Q13766	01-NOV-1996 (TREMREL. 01, LAST SEQUENCE UPDATE)		
DT 01-NOV-1996	01-JAN-1999 (TREMREL. 09, LAST ANNOTATION UPDATE)		
DE ATRIAL NATRIURETIC FACTOR PRECURSOR.			
OS OS EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA; PRIMATES;			
OC CATARRHINI; HOMINIDAE; HOMO.			
RN [1]	SEQUENCE FROM N.A.		
RP MEDLINE; 85206210.			
RA DUBY A.C., CHOI E., GRAHAM R.M., SEIDMAN J.G.;			
RT "Molecular studies of the atrial natriuretic factor gene."			
RL HYPERTENSION 7:31-34(1985).			
DR EMBL; M54947; G178638; -			
DR EMBL; M54951; G178638; JOINED.			
DR PROSITE; PS00263; NATRIURETIC_PEPTIDE; 1.			
DR PFAM; PF00212; ANP; 1.			
KW VASOACTIVE; SIGNAL.			
FT SIGNAL	1 25		
FT PEPTIDE	26 55		
FT PEPTIDE	124 151		
FT DISULFID	130 146		
SQ SEQUENCE	151 AA; 16381 MW; E8827DA3 CRC32;		
Query Match	Score 101; DB 4; Length 151;		
Best Local Similarity	100.0%; Pred. No. 1.40e-08;		
Matches	15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;		
Db 115 LRALLTAPRSLRRSS 129			
Qy 1 LRALLTAPRSLRRSS 15			
RESULT 2	PRELIMINARY;	PRT;	152 AA.
ID Q46540	01-JUN-1998 (TREMREL. 06, CREATED)		
AC Q46540	01-JUN-1998 (TREMREL. 06, LAST SEQUENCE UPDATE)		
DT 01-JUN-1998	01-AUG-1998 (TREMREL. 07, LAST ANNOTATION UPDATE)		
DE ATRIAL NATRIURETIC PEPTIDE.			

```

GN ANP.
OS OVIS ARIES (SHEEP).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA;
OC ARTIODACTYLA; RUMINANTIA; PECORA; BOVOIDEA; CAPRINAE; OVIS.
RN [1]
RP SEQUENCE FROM N.A.
RA AITKEN G.D., RAIZIS A.M., GEORGE P.M., ESPINER E.A., CAMERON V.A.;
RL SUBMITTED (DEC-1997) TO EMBL/GENBANK/DBJ DATA BANKS.
DR EMBL: AF037465; G2708650; -.
DR PROSITE: PS00263; NATRIURETIC_PEPTIDE; 1.
SQ SEQUENCE 152 AA; 16368 MW; D5360BCC CRC32;

Query Match 100.0%; Score 101; DB 6; Length 152;
Best Local Similarity 100.0%; Pred. No. 1.40e-08;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 114 LRLLTAPRSLRRSS 128
QY 1 LRLLTAPRSLRRSS 15

RESULT 3
ID Q29130 PRELIMINARY; PRT; 155 AA.
AC Q29130;
DT 01-NOV-1996 (TREMBLREL. 01, CREATED)
DT 01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)
DT 01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)
DE CARDIODILATIN, ATRIAL NATRIURETIC PEPTIDE.
OS TUPAIA BELANGERI.
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA;
OC SCANDENTIA; TUPAIDAE; TUPAIA.
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=HEART;
RA SCHNEIDEMANN S., MARGERT H.J., FORSSMANN W.G.;
RL SUBMITTED (MAR-1996) TO EMBL/GENBANK/DBJ DATA BANKS.
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=HEART;
RA PARDIGOL A.;
RL SUBMITTED (MAR-1996) TO EMBL/GENBANK/DBJ DATA BANKS.
DR EMBL: Z70294; E233859; -.
DR PROSITE: PS00263; NATRIURETIC_PEPTIDE; 1.
DR PFAM: PF00212; ANP; 1.
SQ SEQUENCE 155 AA; 16860 MW; 77E8CA8B CRC32;

Query Match 93.1%; Score 94; DB 6; Length 155;
Best Local Similarity 86.7%; Pred. No. 5.26e-07;
Matches 13; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Db 117 LRAMLAAPRSLRRSS 131
QY 1 LRLLTAPRSLRRSS 15

RESULT 4
ID Q27778 PRELIMINARY; PRT; 196 AA.
AC Q27778;
DT 01-JAN-1998 (TREMBLREL. 05, CREATED)
DT 01-JAN-1998 (TREMBLREL. 05, LAST SEQUENCE UPDATE)
DT 01-AUG-1998 (TREMBLREL. 07, LAST ANNOTATION UPDATE)
DE CYTOCHROME C-TYPE BIOGENESIS PROTEIN.
GN MTH1746.
OS METHANOBACTERIUM THERMOAUTOTROPHICUM.
OC ARCHAEA; EURVARCHAEOTA; METHANOBACTERIALES; METHANOBACTERIACEAE;
OC METHANOBACTERIUM.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=DELTA H;
RX MEDLINE: 98037514.
RA SMITH D.R., DOUCETTE-STAMM L.A., DELOUGHERY C., LEE H.-M., DUBOIS J.,
RA ALDREDGE T., BASHIRZADEH R., BLAKELY D., COOK R., GILBERT K.,
RA HARRISON D., HOANG L., KEAGLE P., LUMM W., POTIER B., QIU D.,
RA SPADAFORA R., VICARE R., WANG Y., WIERZBOWSKI J., GIBSON R.,
RA JIWANI N., CARUSO A., BUSH D., SAFER H., PATWELL D., PRABHAKAR S.,
RA MDOUGALL S., SHIMER G., GOYAL A., PIETROVSKI S., CHURCH G.M.,
RA DANIELS C.J., MAO J.-I., RICE P., NOLLING J., REEVE J.N.;
RT "Complete genome sequence of Methanobacterium thermoautotrophicum
deltaH: functional analysis and comparative genomics.";
RL J. BACTERIOL. 179:7135-7155(1997).
DR EMBL: AE000930; G2622878; -.
SQ SEQUENCE 196 AA; 21469 MW; CA13344D CRC32;

Query Match 64.4%; Score 65; DB 1; Length 196;
Best Local Similarity 53.3%; Pred. No. 5.20e-01;
Matches 8; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

Db 163 LRLLRGRSDIRRS 177
QY 1 LRLLTAPRSLRRSS 15

RESULT 5
ID Q77443 PRELIMINARY; PRT; 1218 AA.
AC Q77443;
DT 01-NOV-1998 (TREMBLREL. 08, CREATED)
DT 01-NOV-1998 (TREMBLREL. 08, LAST SEQUENCE UPDATE)
DT 01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)
DE VALYL TRNA SYNTHETASE.
OS GIARDIA INTESTINALIS.
OC EUKARYOTA; DIPLOMONADIDA; HEXAMITIDAE; GIARDINAE; GIARDIA.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=WB;
RX MEDLINE: 98284022.
RA HASHIMOTO T., SANCHEZ L.B., SHIRAKURA T., MULLER M., HASEGAWA M.;
RT "Secondary absence of mitochondria in Giardia lamblia and Trichomonas
vaginalis revealed by valyl-trna synthetase phylogeny.";
RL PROC. NATL. ACAD. SCI. U.S.A. 95:6860-6865(1998).
DR EMBL: AB008525; D1029779; -.
KW AMINOACYL-TRNA SYNTHASE.
SQ SEQUENCE 1218 AA; 139225 MW; E98D0361 CRC32;

Query Match 62.4%; Score 63; DB 5; Length 1218;
Best Local Similarity 58.3%; Pred. No. 1.22e+00;
Matches 7; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

Db 1062 LKPLMTAARLR 1073
QY 1 LRLLTAPRSLR 12

RESULT 6
ID Q06308 PRELIMINARY; PRT; 215 AA.
AC Q06308;
DT 01-JUL-1997 (TREMBLREL. 04, CREATED)
DT 01-JUL-1997 (TREMBLREL. 04, LAST SEQUENCE UPDATE)
DT 01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)
DE HYPOTHETICAL 23.1 KD PROTEIN.
GN MTCY13E10.20.
OS MYCOBACTERIUM TUBERCULOSIS.
OC BACTERIA; FIRMICUTES; ACTINOBACTERIA; ACTINOBACTERIDAE;
OC ACTINOMYCETALES; CORYNEBACTERIACEAE; MYCOBACTERIACEAE; MYCOBACTERIUM.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=H37RV;
RA GENTLES S., CHURCHER C.M.;
RL SUBMITTED (MAY-1997) TO EMBL/GENBANK/DBJ DATA BANKS.
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=H37RV;
RA BARRELL B.G., RAJANDREAM M.A., PARKHILL J.;
RL SUBMITTED (MAY-1996) TO EMBL/GENBANK/DBJ DATA BANKS.
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=H37RV;

```


RX MEDLINE; 96181548.
 RA PHILIPP W.J., POULET S., EIGLMEIER K., PASCOPELLA L.,
 RA BALASUBRAMANIAN V., HEYM B., BERCH S., BLOOM B.R., JACOBS W.R. JR.,
 RA COLE S.T.;
 RT "An integrated map of the genome of the tubercle bacillus,
 RT Mycobacterium tuberculosis H37Rv, and comparison with Mycobacterium
 RT leprae";
 RL PROC. NATL. ACAD. SCI. U.S.A. 93:3132-3137(1996).
 DR EMBL: 295324; E315475;
 KW HYPOTHETICAL PROTEIN.
 SO SEQUENCE 215 AA; 23102 MW; FDF01C28 CRC32;

Query Match 60.4%; Score 61; DB 2; Length 215;
 Best Local Similarity 53.3%; Pred. No. 2.83e+00;
 Matches 8; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

Db 189 LRGVAAAPRVRST 203
 QY 1 LRALLTAPRSLRRSS 15

RESULT 7 PRELIMINARY; PRT; 216 AA.
 ID P97981;
 AC P97981;
 DT 01-MAY-1997 (TREMBLREL. 03, CREATED)
 DT 01-MAY-1997 (TREMBLREL. 03, LAST SEQUENCE UPDATE)
 DT 01-AUG-1998 (TREMBLREL. 07, LAST ANNOTATION UPDATE)
 DE 70-KDA HEAT SHOCK PROTEIN (FRAGMENT).
 GN HSP70.
 OS UNIDENTIFIED SOIL ORGANISM.
 OC UNCLASSIFIED; ENVIRONMENTAL SAMPLES.
 RN [1]
 RC SEQUENCE FROM N.A.
 RA YAP W.H., LI X., SOONG T.W., DAVIES J.E.;
 RL SUBMITTED (FEB-1996) TO EMBL/GENBANK/DBJ DATA BANKS.
 DR EMBL: U49150; G1854635;
 KW HEAT SHOCK.
 FT NON_TER 1 1
 FT NON_TER 216 216
 SO SEQUENCE 216 AA; 23489 MW; 106DD33C CRC32;

Query Match 60.4%; Score 61; DB 12; Length 216;
 Best Local Similarity 58.3%; Pred. No. 2.83e+00;
 Matches 7; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Db 97 KDLTSPALRR 108
 QY 2 RALLTAPRSLRR 13

RESULT 8 PRELIMINARY; PRT; 373 AA.
 ID O33426;
 AC O33426;
 DT 01-JAN-1998 (TREMBLREL. 05, CREATED)
 DT 01-JAN-1998 (TREMBLREL. 05, LAST SEQUENCE UPDATE)
 DT 01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)
 DE GLUCOSYLTRANSFERASE I HOMOLOG.
 GN RFAG.
 OS PSEUDOMONAS AERUGINOSA.
 OC BACTERIA; PROTEOBACTERIA; GAMMA SUBDIVISION; PSEUDOMONAS GROUP.
 OC PSEUDOMONAS.
 RN [1]
 RC SEQUENCE FROM N.A.
 RA COYNE M.J., GOLDBERG J.B.;
 RL SUBMITTED (JUL-1996) TO EMBL/GENBANK/DBJ DATA BANKS.
 DR EMBL: U63816; G2226277;
 DR PFAM: PF00534; Glycos_transf_1;
 KW TRANSFERASE.
 SO SEQUENCE 373 AA; 42166 MW; 0551B3E1 CRC32;

Query Match 60.4%; Score 61; DB 2; Length 373;
 Best Local Similarity 46.7%; Pred. No. 2.83e+00;

Matches 7; Conservative 5; Mismatches 3; Indels 0; Gaps 0;
 Db 215 LKALAALPKALRRRT 229
 QY 1 LRALLTAPRSLRRSS 15

RESULT 9 PRELIMINARY; PRT; 246 AA.
 ID P76909;
 AC P76909; P76225;
 DT 01-FEB-1997 (TREMBLREL. 02, CREATED)
 DT 01-FEB-1997 (TREMBLREL. 02, LAST SEQUENCE UPDATE)
 DT 01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)
 DE INNER MEMBRANE PROTEIN MALK.
 OS ESCHERICHIA COLI.
 OC BACTERIA; PROTEOBACTERIA; GAMMA SUBDIVISION; ENTEROBACTERIACEAE;
 OC ESCHERICHIA.
 RN [1]
 RC SEQUENCE FROM N.A.
 RA STRAIN-K12.
 RX MEDLINE; 97251357.
 RA AIBA H., BABA T., FUJITA K., HAYASHI K., INADA T., ISONO K., ITOH T.,
 RA KASAI H., KASHIMOTO K., KIMURA S., KITAKAWA M., KITAGAWA M.,
 RA MAKINO K., MIKI T., MIZOBUCHI K., MORI H., MORI T., MOTOMURA K.,
 RA NAKADE S., NAKAMURA Y., NASHIMOTO H., NISHIO Y., OSHIMA T., SAITO N.,
 RA SAMPEI G., SEKI Y., SIVASUNDARAM S., TAGAMI H., TAKEDA J.,
 RA TAKEMOTO K., TAKEUCHI Y., WADA C., YAMAMOTO Y., HORIUCHI T.;
 RT "A 570-Kb DNA sequence of the Escherichia coli K-12 genome
 RT corresponding to the 28.0-40.1 min region on the linkage map";
 RL DNA RES. 3:363-377(1996).
 RN [2]
 RC SEQUENCE OF 30-246 FROM N.A.
 RA STRAIN-K-12;
 RX MEDLINE; 97426617.
 RA BLATTNER F.R., PLUNKETT III G., BLOCH C.A., PERNA N.T., BURLAND V.,
 RA RILEY M., COLLADO-VIDES J., GLASNER J.D., RODE C.K., MAYHEW G.F.,
 RA GREGOR J., DAVIS N.W., KIRKPATRICK H.A., GOEDEN M.A., ROSE D.J.,
 RA MAU B., SHAO Y.;
 RT "The complete genome sequence of Escherichia coli K-12";
 RL SCIENCE 277:1453-1474(1997).
 DR EMBL: D90819; G1742866;
 DR EMBL: AE000270; G1788053;
 DR PFAM: PF00005; ABC_tran; 1.
 SQ SEQUENCE 246 AA; 27349 MW; 32F5AC45 CRC32;

Query Match 59.4%; Score 60; DB 2; Length 246;
 Best Local Similarity 63.6%; Pred. No. 4.28e+00;
 Matches 7; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Db 174 LRALLAQPRL 184
 QY 1 LRALLTAPRSL 11

RESULT 10 PRELIMINARY; PRT; 303 AA.
 ID O52554;
 AC O52554;
 DT 01-JUN-1998 (TREMBLREL. 06, CREATED)
 DT 01-JUN-1998 (TREMBLREL. 06, LAST SEQUENCE UPDATE)
 DT 01-AUG-1998 (TREMBLREL. 07, LAST ANNOTATION UPDATE)
 DE KINASE.
 GN RIFN.
 OS AMYCOLATOPSIS MEDITERRANEI.
 OC BACTERIA; FIRMICUTES; ACTINOBACTERIA; ACTINOBACTERIACEAE;
 OC ACTINOMYCETALES; PSEUDONOCARDIACEAE; PSEUDONOCARDIACEAE; AMYCOLATOPSIS.
 RN [1]
 RC SEQUENCE FROM N.A.
 RA STRAIN-S699;
 RA KIM C.G., YU T.W., FRYHLE C., HANDA S., FLOSS H.G.;
 RL J. BIOL. CHEM. 0:0-0(1998).
 RN [2]
 RC SEQUENCE FROM N.A.
 RA STRAIN-S699;

RA AUGUST P.R., TANG L., YOON Y.J., NING S., MUELLER R., YU T.W.,
 RA TAYLOR M., HOFFMANN D., KIM C.G., ZHANG X., HUTCHINSON C.R.,
 RA FLOSS H.G.,
 RL CHEM. BIOL. 5:0-0(0002).
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN-S659;
 RA AUGUST P.R., TANG L., YOON Y.J., NING S., MUELLER R., HUTCHINSON C.R.,
 RA FLOSS H.G.,
 RL SUBMITTED (DEC-1997) TO EMBL/GENBANK/DBJ DATA BANKS.
 DR EMBL; AF040570; G2792326;
 SQ SEQUENCE 303 AA; 30823 MW; FEA9BD1 CRC32;
 Query Match 59.4%; Score 60; DB 2; Length 303;
 Best Local Similarity 53.3%; Pred. No. 4.28e+00;
 Matches 8; Conservative 5; Mismatches 2; Indels 0; Gaps 0;
 Db 178 LOALASGPATLRAS 192
 QY 1 LRLLTAPRSLRSS 15
 RESULT 11
 ID Q68404 PRELIMINARY; PRT; 642 AA.
 AC Q68404;
 DT 01-NOV-1996 (TREMBLREL. 01, CREATED)
 DT 01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)
 DT 01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)
 DE ORF UL150.
 OS HUMAN CYTOMEGALOVIRUS.
 OC VIRUSES; DSDNA VIRUSES, NO RNA STAGE; HERPESVIRIDAE; BETAHERPESVIRINAE;
 RN CYTOMEGALOVIRUS.
 RC SEQUENCE FROM N.A.
 RP STRAIN-TOLEDO;
 RX MEDLINE; 96059416.
 RA CHA T.A., TOM E., KEMBLE G.W., DUKE G.M., MOCARSKI E.S., SPAETE R.R.;
 RT "Human cytomegalovirus clinical isolates carry at least 19 genes not
 RT found in laboratory strains."
 RL J. VIROL. 70:78-83(1996).
 DR EMBL; U33331; G1167937;
 SQ SEQUENCE 642 AA; 70848 MW; 503B0F4B CRC32;
 Query Match 59.4%; Score 60; DB 14; Length 642;
 Best Local Similarity 53.3%; Pred. No. 4.28e+00;
 Matches 8; Conservative 3; Mismatches 4; Indels 0; Gaps 0;
 Db 44 LRLLTTRRELPRTP 58
 QY 1 LRLLTAPRSLRSS 15
 RESULT 12
 ID Q61790 PRELIMINARY; PRT; 227 AA.
 AC Q61790;
 DT 01-AUG-1998 (TREMBLREL. 07, CREATED)
 DT 01-AUG-1998 (TREMBLREL. 07, LAST SEQUENCE UPDATE)
 DT 01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)
 DE R12E2.11 PROTEIN.
 GN R12E2.11.
 OS CAENORHABDITIS ELEGANS.
 OC EUKARYOTA; METAZOA; NEMATODA; SECERNENTEA; RHABDITIA; RHABDITIDA;
 RN RHABDITIA; RHABDITOIDEA; RHABDITIDAE; PELODERINAE; CAENORHABDITIS.
 RC SEQUENCE FROM N.A.
 RP STRAIN-BRISTOL N2;
 RX MEDLINE; 94150718.
 RA WILSON R., AINSOUGH R., ANDERSON K., BAYNES C., BERKS M.,
 RA BONFIELD J., BURTON J., CONNELL M., COPSEY T., COOPER J., COULSON A.,
 RA CRAXTON M., DEAN S., DU Z., DURBIN R., FAVELLO A., FULTON L.,
 RA GARDNER A., GREEN P., HAWKINS T., HILLIER L., JIER M., JOHNSTON L.,
 RA JONES M., KERSHAW J., KIRSTEN J., LAISTER N., LATREILLE P.,
 RA LIGHTING J., LLOYD C., MCMURRAY A., MORTIMORE B., O'CALLAGHAN M.,

RA PARSONS J., PERCY C., RIEKEN L., ROOPRA A., SAUNDERS D., SHOWNKEEN R.,
 RA SHALDON N., SMITH A., SONNHAMMER E., STADEN R., SULSTON J.,
 RA THIERRY-MIEG J., THOMAS K., VAUDIN M., VAUGHAN K., WATERSTON R.,
 RA WATSON A., WEINSTOCK L., WILKINSON-SPROAT J., WORLDMAN P.,
 RT "2.2 Mb of contiguous nucleotide sequence from chromosome III of C.
 RT elegans."
 RL NATURE 368:32-38(1994).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN-BRISTOL N2;
 RA WATERSTON R.;
 RA GOELA D., SCHEET P.;
 RL SUBMITTED (MAY-1998) TO EMBL/GENBANK/DBJ DATA BANKS.
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN-BRISTOL N2;
 RL WATERSTON R.;
 CC -1- SIMILARITY: PARTIAL WITH OTHER PHOSPHORIBOSYLTRANSFERASE ALSO
 CC INVOLVED IN BIOSYNTHESIS OR SALVAGE OF PURINES OR PYRIMIDINES.
 DR EMBL; AF067219; G3150523;
 DR PROSITE; PS00103; PUR_PYR_PR_TRANSFER; 1.
 KW TRANSFERASE; GLYCOSYLTRANSFERASE.
 SQ SEQUENCE 227 AA; 25192 MW; AD1ED310 CRC32;
 Query Match 58.4%; Score 59; DB 5; Length 227;
 Best Local Similarity 40.0%; Pred. No. 6.44e+00;
 Matches 6; Conservative 6; Mismatches 3; Indels 0; Gaps 0;
 Db 62 LRRIMSPRVLRMAA 76
 QY 1 LRLLTAPRSLRSS 15
 RESULT 13
 ID Q96517 PRELIMINARY; PRT; 348 AA.
 AC Q96517;
 DT 01-FEB-1997 (TREMBLREL. 02, CREATED)
 DT 01-FEB-1997 (TREMBLREL. 02, LAST SEQUENCE UPDATE)
 DT 01-JAN-1999 (TREMBLREL. 09, LAST ANNOTATION UPDATE)
 DE MAP KINASE KINASE ALPHA PROTEIN KINASE (EC 2.7.1.37)
 DE (PHOSPHORYLASE B KINASE KINASE) (GLYCOCEN SYNTHASE A KINASE)
 DE (HYDROXYALKYL-PROTEIN KINASE) (SERINE(THREONINE) PROTEIN KINASE).
 GN MAP2KALPHA.
 OS ARABIDOPSIS THALIANA (MOUSE-EAR CRESS).
 OC EUKARYOTA; VIRIDIPANTAE; STREPTOPHYTA; EMBRYOPHYTA; TRACHEOPHYTA;
 OC EUPHYLLOPHYTES; SPERMATOPHYTA; MAGNOLIOPHYTA; EUDICOTYLEDONS; ROSIDAE;
 OC CAPPARALES; BRASSICACEAE; ARABIDOPSIS.
 RN [1]
 RP SEQUENCE FROM N.A.
 RA JOUANNIC S., HAMAL A., KREIS M., HENRY Y.;
 RL PLANT PHYSIOL. 112:1397-1397(1996).
 DR EMBL; Y07694; E263927;
 DR PFAM; PF00069; pkinase; 1.
 DR MENDEL; 14316; ARATH; 2349.mn14316.
 KW TRANSFERASE; PROTEIN KINASE.
 SQ SEQUENCE 348 AA; 38329 MW; E9A05E6F CRC32;
 Query Match 58.4%; Score 59; DB 10; Length 348;
 Best Local Similarity 46.7%; Pred. No. 6.44e+00;
 Matches 7; Conservative 4; Mismatches 4; Indels 0; Gaps 0;
 Db 334 LRQMLPPRPLPSAS 348
 QY 1 LRLLTAPRSLRSS 15
 RESULT 14
 ID Q80398 PRELIMINARY; PRT; 348 AA.
 AC Q80398;
 DT 01-NOV-1998 (TREMBLREL. 08, CREATED)
 DT 01-NOV-1998 (TREMBLREL. 08, LAST SEQUENCE UPDATE)
 DT 01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)
 DE MAP KINASE KINASE 5.

Search completed: Wed Jun 16 13:20:44 1999
Job time : 40 secs.

WISORLH (TM)

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MSrch_pp protein - protein database search, using Smith-Waterman algorithm

Run on: Wed Jun 16 13:22:42 1999; MasPar time 3.16 Seconds
33.675 Million cell updates/sec

Tabular output not generated.

Title: >US-09-027-777B-3
Description: (1-5) from US0902777B.pap
Perfect Score: 41
Sequence: 1 NSFRY 5

Scoring table: PAM 150
Gap 15

Searched: 170751 seqs, 2126608 residues

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database: a-geneseq35
1:part1 2:part2 3:part3 4:part4 5:part5 6:part6 7:part7
8:part8 9:part10 11:part11 12:part12 13:part13
14:part14 15:part15 16:part16 17:part17 18:part18
19:part19 20:part20 21:part21 22:part22 23:part23
24:part24 25:part25 26:part26 27:part27 28:part28
29:part29 30:part30 31:part31 32:part32 33:part33
34:part34 35:part35 36:part36 37:part37 38:part38
39:part39

Statistics: Mean 14.664; Variance 41.977; scale 0.349

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description	Pred. No.
1	41	100.0	22	5	R29918	2.82e+02
2	41	100.0	22	35	W70089	2.82e+02
3	41	100.0	22	1	P81568	2.82e+02
4	41	100.0	22	7	R40675	2.82e+02
5	41	100.0	22	7	R40674	2.82e+02
6	41	100.0	23	7	R36974	2.82e+02
7	41	100.0	23	7	R36973	2.82e+02
8	41	100.0	23	7	P71448	2.82e+02
9	41	100.0	23	7	R40663	2.82e+02
10	41	100.0	23	7	R36971	2.82e+02
11	41	100.0	23	7	R40654	2.82e+02
12	41	100.0	23	1	P82984	2.82e+02
13	41	100.0	24	1	P94851	2.82e+02
14	41	100.0	24	1	R04102	2.82e+02
15	41	100.0	25	7	R40702	2.82e+02
16	41	100.0	25	7	R40456	2.82e+02

17	41	100.0	25	7	R40563	2.82e+02
18	41	100.0	25	7	R40440	2.82e+02
19	41	100.0	25	7	R40475	2.82e+02
20	41	100.0	25	7	R40569	2.82e+02
21	41	100.0	25	7	R40423	2.82e+02
22	41	100.0	25	7	R36951	2.82e+02
23	41	100.0	25	7	R36952	2.82e+02
24	41	100.0	25	7	R40412	2.82e+02
25	41	100.0	26	3	R21586	2.82e+02
26	41	100.0	26	3	R21587	2.82e+02
27	41	100.0	26	2	P71129	2.82e+02
28	41	100.0	26	3	R21582	2.82e+02
29	41	100.0	26	3	R21583	2.82e+02
30	41	100.0	27	12	R62357	2.82e+02
31	41	100.0	27	12	R62358	2.82e+02
32	41	100.0	27	3	P60084	2.82e+02
33	41	100.0	28	5	R25947	2.82e+02
34	41	100.0	28	3	P50048	2.82e+02
35	41	100.0	28	35	W70087	2.82e+02
36	41	100.0	28	35	W70088	2.82e+02
37	41	100.0	28	2	P61015	2.82e+02
38	41	100.0	28	1	P91314	2.82e+02
39	41	100.0	28	1	R03415	2.82e+02
40	41	100.0	28	3	P61706	2.82e+02
41	41	100.0	32	36	W67039	2.82e+02
42	41	100.0	35	2	R08327	2.82e+02
43	41	100.0	43	1	P81211	2.82e+02
44	41	100.0	126	2	R00582	2.82e+02
45	41	100.0	151	3	P50050	2.82e+02

ALIGNMENTS

RESULT 1
ID R29918 standard; Protein; 22 AA.
AC R29918;
DT 21-JAN-1993 (first entry)
DE CNP analogue (26).
KW C-type natriuretic peptide; smooth muscle; stenosis; angiotensin;
KW arteriosclerosis; alpha-hANP; A-type natriuretic peptide; GMP;
KW CNP-22.
OS Synthetic.
FH Key Location/Qualifiers
FT modified_site 2 /note= "pNO2F-Phe"
FT region 7..22 /note= "alpha-hANP derived residues"
FT disulfide_bond 1..22.
PN EP-497368-A.
PD 05-AUG-1992.
PF 31-JAN-1992; 101621.
PR 31-JAN-1991; JP-011321.
PR 28-JUN-1991; JP-254066.
PA (MATSUO) MATSUO H.
PA (SUNR) SUNTORY LTD.
PI Furuya M, Kitajima Y, Matsuo H, Minamitake Y, Tanaka S;
DR WPI, 92-260818/32.
PT New C-type natriuretic peptide analogues - suppress growth of
PT vascular smooth muscle cells, for treatment and prevention of
PT arteriosclerosis
PS Disclosure; Page 7; 20pp; English.
CC in the determination which domain structure of CNP was responsible
CC for the cyclic GMP producing activity characteristic of CNP, the
CC peptides of R25948-36, R29720-31 and R29914-19 were synthesized.
CC It was found that CNP derivs. exhibiting a stronger cyclic GMP
CC producing activity than CNP-22 or alpha-hANP could be constructed
CC by replacing part of the amino acid residues in CNP-22, CNP (6-22)
CC and [Leu10, Lys11, Leu12] alpha-hANP(7-28) with unusual amino acid
CC (non-native type) residues.
CC CNP derivs. that exhibit a strong cyclic GMP producing activity and
CC cell growth suppressing activity against vascular smooth muscle cells
CC are anticipated to be useful in therapeutics or preventives against
CC diseases such as stenosis and arteriosclerosis. Among the derivs.

CC that contain unusual amino acid (non-native type) derivs. would
 CC probably exhibit resistance to proteases in the living body (in blood
 CC and on the surface of cells) upon admin. in vivo. Therefore, those
 CC derivs. even if they have a lower cyclic GMP producing activity than
 CC CNP-22 or alpha-hANP, would be characterised by a longer blood half-
 CC life than CNP analogs free from unusual amino acids, and, from this
 CC viewpoint, too, those derivs. are anticipated to have industrial
 CC utility.
 CC Cyclic GMP producing activity for CNP analog (26) is 255% increase
 CC for 1 microm, compared to 100% for alpha-hANP and 621% for CNP-22
 CC (specific activity as compared to the activity of 1 microm alpha-hANP
 CC (2000 fmol/400000 cells), with max. activity being equiv. to the
 CC cyclic GMP producing ability of each cpd. for 1 microm.
 SQ Sequence 22 AA;

Query Match 100.0%; Score 41; DB 5; Length 22;
 Best Local Similarity 100.0%; Pred. No. 2.82e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Db 18 nsfry 22
 |||||
 Qy 1 NSFry 5

RESULT 2
 ID W70089 standard; peptide: 22 AA.
 AC W70089;
 DT 28-OCT-1998 (first entry)
 DE Alpha human atrial natriuretic peptide (alpha-hANP) 2 (residues 7-28).
 KW ANP: atrial natriuretic peptide; cardiac disease; cardiac hypertrophy;
 KW chronic heart failure; ischaemic cardiac disease; arrhythmia;
 KW CGMP: pulmonary blood circulation; haemodynamic property.
 OS Homo sapiens.
 PN W09834536-A1.
 PD 13-AUG-1998.
 PF 05-FEB-1998; J00483.
 PR 05-FEB-1997; JP-022594.
 PI (SUNR) SONTORY LTD.
 PI Furuya M, Hidaka T, Inomata N, Yamaki A;
 DR WPI: 98-446949/38.
 PT Drug composition comprises natriuretic peptide(s) - for safe
 PT treatment of cardiac hypertrophy associated diseases and chronic
 PT heart failure
 PS Examples; Page 23; 35pp; Japanese.
 CC This represents a human alpha atrial natriuretic peptide sequence
 CC (alpha-hANP). The invention provides a composition for treating cardiac
 CC diseases associated with cardiac hypertrophy. The composition comprises
 CC an active ingredient capable of binding to the peptide receptor of GC-A
 CC and promoting production of cGMP. The drug composition may be used
 CC clinically to treat cardiac diseases caused by cardiac hypertrophy,
 CC including chronic heart failure, ischaemic cardiac diseases and
 CC arrhythmia. The active substance can bind to the natriuretic peptide
 CC receptor of GC-A and promote production of cGMP, effectively preventing
 CC cardiac hypertrophy and leading to improvement of the pulmonary blood
 CC circulation. The substance does not affect haemodynamic properties,
 CC blood pressure, heart beat and urine volume.
 SQ Sequence 22 AA;

Query Match 100.0%; Score 41; DB 35; Length 22;
 Best Local Similarity 100.0%; Pred. No. 2.82e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Db 18 nsfry 22
 |||||
 Qy 1 NSFry 5

RESULT 3
 ID P81568 standard; protein: 22 AA.
 AC P81568;
 DT 10-OCT-1990 (first entry)
 DE Atrial peptide analog with diuretic and natriuretic activities
 KW Atrial peptide analog; diuretic; natriuretic; hypotensive activity;

KW atriopeptin; alpha-hANP.
 OS Synthetic.
 FH Key Location/Qualifiers
 FT misc_difference 1..1 /label= OTHER
 FT /note="beta-mercaptopropionic acid deriv." 1..17
 FT Disulphide-bonds
 PN US4721704-A.
 PD 26-JAN-1988.
 PF 09-MAY-1986; 861528.
 PR 09-MAY-1986; US-861528.
 PA (PENI-) Peninsula Labs Inc.
 DR WPI: 88-049653/07.
 PT Atrial peptide analogues - are diuretics and hypotensives.
 PS Disclosure; 9pp; English.
 CC Ala at the 3 position is D-Ala. Tyr22 has an NH2 group attached.
 CC The peptide increases the cyclic GMP produced in assayed cells at
 CC considerable greater levels than Atriopeptin III and alpha-hANP.
 CC has a much greater hypotensive effect, and is a more potent diuretic.
 CC See also P81568-P81572.
 SQ Sequence 22 AA;

Query Match 100.0%; Score 41; DB 1; Length 22;
 Best Local Similarity 100.0%; Pred. No. 2.82e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Db 18 nsfry 22
 |||||
 Qy 1 NSFry 5

RESULT 4
 ID R40675 standard; Protein: 22 AA.
 AC R40675;
 DT 14-SEP-1993 (first entry)
 DE [Arg129][D-Ala132][D-Ser148]hANVP(130-145).
 KW Human; pre-pro; atrial natriuretic/vasodilator peptide; ANVP; rat;
 KW regulation; fluid volume; blood pressure.
 OS Synthetic.
 FH Key Location/Qualifiers
 FT disulfide_bond 2..17
 FT misc_difference 4 /note= "D-form residue"
 FT misc_difference 19 /note= "D-form residue"
 FT US212286-A.
 PD 18-MAY-1993.
 PF 09-APR-1984; 602117.
 PR 09-APR-1984; US-602117.
 PR 01-JUN-1984; US-616488.
 PR 08-MAY-1985; US-766030.
 PR 05-JUN-1986; US-870795.
 PA (SCIO-) SCIOS NOVA INC.
 PI Lewicki JA, Scarborough RM;
 DR WPI: 93-175525/21.
 PT New polypeptide cpd. - useful as natriuretic, diuretic and/or
 PT vasodilator in mammals
 PS Disclosure; Column 52; 45pp; English.
 CC The sequences given in R40387-748 are atrial natriuretic/
 CC vasodilator peptide (ANVP) cDNAs. These ANVP fragments may be used
 CC for regulation of fluid volume and blood pressure in host organisms.
 CC These ANVP fragments may be produced by solid-phase techniques. See
 CC also R36937-78
 SQ Sequence 22 AA;

Query Match 100.0%; Score 41; DB 7; Length 22;
 Best Local Similarity 100.0%; Pred. No. 2.82e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Db 18 nsfry 22
 |||||
 Qy 1 NSFry 5

```

RESULT 5
ID R40674 standard; Protein; 22 AA.
AC R40674;
DT 14-SEP-1993 (first entry)
DE [Arg128][D-Ala131][D-Ser147]rANVP(129-145)-NH2.
KW Human; pre-pro; atrial natriuretic/vasodilator peptide; ANVP; rat;
KW regulation; fluid volume; blood pressure.
OS Synthetic.
FH Key Location/Qualifiers
FT disulfide_bond 2..17
FT misc_difference 4 /note= "D-form residue"
FT misc_difference 19 /note= "D-form residue"
FT modified_site 22 /note= "Amidated C terminal"
PN US5212286-A.
PD 18-MAY-1993.
PF 09-APR-1984; 602117.
PR 09-APR-1984; US-602117.
PR 01-JUN-1984; US-616488.
PR 08-MAY-1985; US-766030.
PR 05-JUN-1986; US-870795.
PA (SCIO-) SCIOS NOVA INC.
PI Lewicki JA, Scarborough RM;
DR WPI; 93-175525/21.
PT New polypeptide cpd. - useful as natriuretic, diuretic and/or
PT vasodilator in mammals
PS Disclosure; Column 51; 45pp; English.
CC The sequences given in R40387-748 are atrial natriuretic/
CC vasodilator peptide (ANVP) cDNAs. These ANVP fragments may be used
CC for regulation of fluid volume and blood pressure in host organisms.
CC These ANVP fragments may be produced by solid-phase techniques. See
CC also R36937-78.
SQ Sequence 22 AA;

Query Match 100.0%; Score 41; DB 7; Length 22;
Best Local Similarity 100.0%; Pred. No. 2.82e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 18 nsfry 22
QY 1 NSFRY 5

RESULT 6
ID R36974 standard; Protein; 23 AA.
AC R36974;
DT 14-SEP-1993 (first entry)
DE ANVP #38
KW Human; pre-pro; atrial natriuretic/vasodilator peptide; ANVP; rat;
KW regulation; fluid volume; blood pressure.
OS Synthetic.
FH Key Location/Qualifiers
FT disulfide_bond 2..18
FT misc_difference 2 /note= "D-form residue"
PN US5212286-A.
PD 18-MAY-1993.
PF 09-APR-1984; 602117.
PR 09-APR-1984; US-602117.
PR 01-JUN-1984; US-616488.
PR 08-MAY-1985; US-766030.
PR 05-JUN-1986; US-870795.
PA (SCIO-) SCIOS NOVA INC.
PI Lewicki JA, Scarborough RM;
DR WPI; 93-175525/21.
PT New polypeptide cpd. - useful as natriuretic, diuretic and/or
PT vasodilator in mammals
PS Disclosure; Column 11; 45pp; English.
CC The sequences given in R36937-78 are atrial natriuretic/vasodilator
CC peptide (ANVP) cDNAs. These ANVP fragments may be used for regulation
CC of fluid volume and blood pressure in host organisms. See also
CC R40387-749.
SQ Sequence 23 AA;

Query Match 100.0%; Score 41; DB 7; Length 23;
Best Local Similarity 100.0%; Pred. No. 2.82e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 19 nsfry 23
QY 1 NSFRY 5

RESULT 7
ID R36973 standard; Protein; 23 AA.
AC R36973;
DT 14-SEP-1993 (first entry)
DE ANVP #37.
KW Human; pre-pro; atrial natriuretic/vasodilator peptide; ANVP; rat;
KW regulation; fluid volume; blood pressure.
OS Synthetic.
FH Key Location/Qualifiers
FT disulfide_bond 2..18
FT misc_difference 3 /note= "D-form residue"
PN US5212286-A.
PD 18-MAY-1993.
PF 09-APR-1984; 602117.
PR 09-APR-1984; US-602117.
PR 01-JUN-1984; US-616488.
PR 08-MAY-1985; US-766030.
PR 05-JUN-1986; US-870795.
PA (SCIO-) SCIOS NOVA INC.
PI Lewicki JA, Scarborough RM;
DR WPI; 93-175525/21.
PT New polypeptide cpd. - useful as natriuretic, diuretic and/or
PT vasodilator in mammals
PS Disclosure; Column 11; 45pp; English.
CC The sequences given in R36937-78 are atrial natriuretic/vasodilator
CC peptide (ANVP) cDNAs. These ANVP fragments may be used for regulation
CC of fluid volume and blood pressure in host organisms. These ANVP
CC fragments may be produced by solid-phase techniques. See also
CC R40387-749.
SQ Sequence 23 AA;

Query Match 100.0%; Score 41; DB 7; Length 23;
Best Local Similarity 100.0%; Pred. No. 2.82e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 19 nsfry 23
QY 1 NSFRY 5

RESULT 8
ID P71448 standard; peptide; 23 AA.
AC P71448;
DT 01-MAY-1991 (first entry)
DE Natriuretic peptide.
KW Diuretic; atrial natriuretic facotr; ANF; hypotensive agent;
KW hypertension; vasodilation.
OS Synthetic.
FT Modified_site 1 /label= D-Tyr
FT disulfide_bond 2..18
PN EP-246795-A.
PD 25-NOV-1987.
PF 11-MAY-1987; 304163.
PR 20-MAY-1986; CA-509564.
PA (ADPE-) ADV PEPTIDE DEV LTD.
PI Deghenghi R, Immer HU;
DR WPI; 87-329003/47.

CC of fluid volume and blood pressure in host organisms. These ANVP
CC fragments may be produced by solid-phase techniques. See also
CC R40387-749.
SQ Sequence 23 AA;

Query Match 100.0%; Score 41; DB 7; Length 23;
Best Local Similarity 100.0%; Pred. No. 2.82e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 19 nsfry 23
QY 1 NSFRY 5
```

PT New synthetic natriuretic peptide(s) - contg. 23 amino acid(s) and
 PT having eg diuretic, vaso-relaxant and antihypertensive
 PT activities.
 PS Claim 5; Page 16; 16pp; English.
 CC The peptide shows dissociation of diuretic and natriuretic
 CC effects from undesirable vasorelaxant effects on the heart rate,
 CC and duration of action is longer than for known natriuretic
 CC peptides. It is prep'd. by solid phase synthesis. The C-terminal
 CC has an OH or NH₂ gp.
 CC See also P71447.
 SQ Sequence 23 AA;

Query Match 100.0%; Score 41; DB 2; Length 23;
 Best Local Similarity 100.0%; Pred. No. 2.82e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 19 nsfry 23
 |||||
 QY 1 NSFRY 5

RESULT 9

ID R40663 standard; Protein; 23 AA.
 AC R40663;
 DT 14-SEP-1993 (first entry)
 DE [Arg129][D-Ala132][D-Cys146]hANVP(130-151).
 KW Human; pre-pro; atrial natriuretic/vasodilator peptide; ANVP; rat;
 KW regulation; fluid volume; blood pressure.
 OS Synthetic.

FH Key Location/Qualifiers
 FT disulfide_bond 2..18
 FT misc_difference 4
 FT misc_difference 18 /note= "D-form residue"
 FT /note= "D-form residue"

PN US5212286-A.
 PD 18-MAY-1993.
 PF 09-APR-1984; 602117.
 PR 09-APR-1984; US-602117.
 PR 01-JUN-1984; US-616488.
 PR 08-MAY-1985; US-766030.
 PR 05-JUN-1986; US-870795.
 PA (SCIO-) SCIOS NOVA INC.
 PI Lewicki JA, Scarborough RM;
 DR WPI; 93-175525/21.
 PT New polypeptide cpd. - useful as natriuretic, diuretic and/or
 PT vasodilator in mammals
 PS Disclosure; Column 50; 45pp; English.
 CC The sequences given in R40387-748 are atrial natriuretic/
 CC vasodilator peptide (ANVP) cDNAs. These ANVP fragments may be used
 CC for regulation of fluid volume and blood pressure in host organisms.
 CC These ANVP fragments may be produced by solid-phase techniques. See
 CC also R36937-78.
 SQ Sequence 23 AA;

Query Match 100.0%; Score 41; DB 7; Length 23;
 Best Local Similarity 100.0%; Pred. No. 2.82e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 19 nsfry 23
 |||||
 QY 1 NSFRY 5

RESULT 10

ID R36971 standard; Protein; 23 AA.
 AC R36971;
 DT 14-SEP-1993 (first entry)
 DE ANVP #35.
 KW Human; pre-pro; atrial natriuretic/vasodilator peptide; ANVP; rat;
 KW regulation; fluid volume; blood pressure.
 OS Synthetic.

FH Key Location/Qualifiers

FT disulfide_bond 2..18
 FT misc_difference 6 /note= "D-form residue"
 PN US5212286-A.
 PD 18-MAY-1993.
 PF 09-APR-1984; 602117.
 PR 09-APR-1984; US-602117.
 PR 01-JUN-1984; US-616488.
 PR 08-MAY-1985; US-766030.
 PR 05-JUN-1986; US-870795.
 PA (SCIO-) SCIOS NOVA INC.
 PI Lewicki JA, Scarborough RM;
 DR WPI; 93-175525/21.
 PT New polypeptide cpd. - useful as natriuretic, diuretic and/or
 PT vasodilator in mammals
 PS Disclosure; Column 50; 45pp; English.
 CC The sequences given in R36937-78 are atrial natriuretic/vasodilator
 CC peptide (ANVP) cDNAs. These ANVP fragments may be used for regulation
 CC of fluid volume and blood pressure in host organisms. These ANVP
 CC fragments may be produced by solid-phase techniques. See also
 CC R40387-749.
 SQ Sequence 23 AA;

Query Match 100.0%; Score 41; DB 7; Length 23;
 Best Local Similarity 100.0%; Pred. No. 2.82e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 19 nsfry 23
 |||||
 QY 1 NSFRY 5

RESULT 11

ID R40654 standard; Protein; 23 AA.
 AC R40654;
 DT 14-SEP-1993 (first entry)
 DE [Arg128][D-Ala131][D-Ala142]ANVP(129-150).
 KW Human; pre-pro; atrial natriuretic/vasodilator peptide; ANVP; rat;
 KW regulation; fluid volume; blood pressure.
 OS Synthetic.

FH Key Location/Qualifiers
 FT disulfide_bond 2..18
 FT misc_difference 4
 FT misc_difference 15 /note= "D-form residue"
 FT /note= "D-form residue"

PN US5212286-A.
 PD 18-MAY-1993.
 PF 09-APR-1984; 602117.
 PR 09-APR-1984; US-602117.
 PR 01-JUN-1984; US-616488.
 PR 08-MAY-1985; US-766030.
 PR 05-JUN-1986; US-870795.
 PA (SCIO-) SCIOS NOVA INC.
 PI Lewicki JA, Scarborough RM;
 DR WPI; 93-175525/21.
 PT New polypeptide cpd. - useful as natriuretic, diuretic and/or
 PT vasodilator in mammals
 PS Disclosure; Column 50; 45pp; English.
 CC The sequences given in R40387-748 are atrial natriuretic/
 CC vasodilator peptide (ANVP) cDNAs. These ANVP fragments may be used
 CC for regulation of fluid volume and blood pressure in host organisms.
 CC These ANVP fragments may be produced by solid-phase techniques. See
 CC also R36937-78.
 SQ Sequence 23 AA;

Query Match 100.0%; Score 41; DB 7; Length 23;
 Best Local Similarity 100.0%; Pred. No. 2.82e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 19 nsfry 23
 |||||
 QY 1 NSFRY 5

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 12
ID P82984 standard; protein; 23 AA.
AC P82984;
DT 05-DEC-1990 (first entry)
DE Alpha-human Atrial Natriuretic Peptide (hANP) analogue #3.
KW alpha-human Atrial Natriuretic Peptide analogue;
OS hypotensive activity.
FH Key Location/Qualifiers
FT disulfide_bond 2..18 /note="intramolecular"
PN EP-269220-A.
PD 01-JUN-1988.
PF 29-SEP-1987; 308586.
PR 29-SEP-1986; JP-231429.
PA (TAKE) Takeda Chemical Ind KK.
PI Fujino M, Wakimasu M, Nishikawa K.;
DR WPI; 88-149016/22.
PT Alpha-hANP peptide analogues -
are hypotensives and natriuretics.
PS Claim 1; page 32; 33pp; English.
CC Peptides can be used as a therapeutic drug for hypertension, a
diuretic, for cardiac and cerebral circulatory diseases and as a
muscle relaxant.
CC See also P82684 and P82983.
SQ Sequence 23 AA;

Query Match 100.0%; Score 41; DB 1; Length 23;
Best Local Similarity 100.0%; Pred. No. 2.82e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DB 19 nsfry 23
|||||
QY 1 NSFry 5

RESULT 13
ID P94851 standard; peptide; 24 AA.
AC P94851;
DT 30-MAR-1992 (first entry)
DE Sequence of atrial natriuretic factor (ANF) analogue.
KW Diuretic; natriuretic; vasodilator; immunomodulator.
FH Key Location/Qualifiers
FT modified_site 1 /label= H-Ser
FT disulfide_bond 3..19
FT modified_site 24 /label= Tyr-OH
FT modified_site 4 /label= Tyr(Me)
PN EP-299397-A.
PD 18-JAN-1989.
PF 09-JUL-1988; 111011.
PR 16-JUL-1987; DE-723551.
PA (FARH) HOECHST AG.
PI Breipohl G, Knollie J, Konig W, Hropot M;
DR WPI; 89-016929/03.
PT New atrial natriuretic factor analogues - useful as vasodilators,
natriuretics, diuretics, immuno-modulators, etc.
PS Example; Page 15; 24pp; German.
CC P93041,P94848-P94853,P93098-P93100 are examples of the generic
formula for peptides of the invention. They have diuretic,
natriuretic and vasodilatory activity, and also immunomodulatory
activity. They may also be used to treat renal insufficiency and to
protect the kidneys against renal toxins, e.g. cyclosporin during
kidney transplantation, and for treating glaucoma and/or reducing
intraocular pressure.
SQ Sequence 24 AA;

Query Match 100.0%; Score 41; DB 4; Length 24;
Best Local Similarity 100.0%; Pred. No. 2.82e+02;

DB 20 nsfry 24
|||||
QY 1 NSFry 5

RESULT 14
ID R04102 standard; peptide; 24 AA.
AC R04102;
DT 10-SEP-1990 (first entry)
DE Intranasally effective diuretic atrial peptide.
KW Diuretic; atrial peptide.
OS Synthetic.
FH Key Location/Qualifiers
FT disulfide_bond 3..19
FT misc_difference 8 /label=May be Ile or Met
PN CA1267086-A.
PD 27-MAR-1990.
PF 9-MAY-1986; 508837.
PR 10-MAY-1985; US-732781.
PA (MONS) Monsanto Co.
PI Klopff LL, Hecht RI;
DR WPI; 90-124666/17.
PT Diuretic compsn. contg. atrial peptide -
in from for nasal admin. pref. in aq. soln.
PS Claim 1; Page 8; 10pp; English.
CC Derivatives of the diuretic peptide may have one or both C-terminal
residues and up to four N-terminal residues absent.
SQ Sequence 24 AA;

Query Match 100.0%; Score 41; DB 1; Length 24;
Best Local Similarity 100.0%; Pred. No. 2.82e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DB 20 nsfry 24
|||||
QY 1 NSFry 5

RESULT 15
ID R40702 standard; Protein; 25 AA.
AC R40702;
DT 14-SEP-1993 (first entry)
DE [Ser136]hANVP(127-151).
KW Human; pre-pro; atrial natriuretic/vasodilator peptide; ANVP; rat;
regulation; fluid volume; blood pressure.
OS Synthetic.
FH Key Location/Qualifiers
FT disulfide_bond 4..20
PN US5212286-A.
PD 18-MAY-1993.
PF 09-APR-1984; 602117.
PR 09-APR-1984; US-602117.
PR 01-JUN-1984; US-618488.
PR 08-MAY-1985; US-766030.
PR 05-JUN-1986; US-870795.
PA (SCIO-) SCIOS NOVA INC.
PI Lewicki JA, Scarborough RM;
DR WPI; 93-175525/21.
PT New polypeptide cpd. - useful as natriuretic, diuretic and/or
vasodilator in mammals
PS Disclosure; Column 54; 45pp; English.
CC The sequences given in R40387-748 are atrial natriuretic/
vasodilator peptide (ANVP) cDNAs. These ANVP fragments may be used
for regulation of fluid volume and blood pressure in host organisms.
CC These ANVP fragments may be produced by solid-phase techniques. See
also R36937-78.
SQ Sequence 25 AA;

Query Match 100.0%; Score 41; DB 7; Length 25;
Best Local Similarity 100.0%; Pred. No. 2.82e+02;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 21 nsfry 25

|||||

QY 1 NSFry 5

Search completed: Wed Jun 16 13:22:58 1999
Job time : 16 secs.

(TM)

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mpsrch_pp  protein - protein database search, using Smith-Waterman algorithm
Run on:      Wed Jun 16 13:25:00 1999;  MasPar time 1.30 seconds
              39.045 Million cell updates/sec
Tabular output not generated.

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Title:
Description:
Perfect Score: 41
Sequence: 1 NSFRY 5
>US-09-027-777B-3
(1-5) from US0902777B.pep

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Scoring table: PAM 150
Gap 15

Searched: 106580 seqs, 10152877 residues

Post-processing: Minimum Match 0%
Listing first 45 summariesDatabase: a-issued
1:5A COMB 2:5B COMB 3:PCT9 COMB 4:backfiles1

Statistics: Mean 13.767; Variance 41.507; scale 0.332

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score			Query Match	Length	DB ID	Description	Pred. No.
	Score	Match						
1	41	100.0	5	4	5212286-22	Patent No. 5212286.	1.48e+02	
2	41	100.0	22	1	US-07-828-Sequence 26, Applicati	1.48e+02		
3	41	100.0	22	1	US-07-828-Sequence 27, Applicati	1.48e+02		
4	41	100.0	23	4	5212286-48	Patent No. 5212286.	1.48e+02	
5	41	100.0	23	4	5212286-47	Patent No. 5212286.	1.48e+02	
6	41	100.0	23	4	5212286-39	Patent No. 5212286.	1.48e+02	
7	41	100.0	23	4	5212286-37	Patent No. 5212286.	1.48e+02	
8	41	100.0	23	4	5212286-43	Patent No. 5212286.	1.48e+02	
9	41	100.0	23	4	5212286-45	Patent No. 5212286.	1.48e+02	
10	41	100.0	23	4	5212286-44	Patent No. 5212286.	1.48e+02	
11	41	100.0	24	1	US-08-257-Sequence 5, Applicatio	1.48e+02		
12	41	100.0	25	4	5212286-55	Patent No. 5212286.	1.48e+02	
13	41	100.0	25	4	5212286-49	Patent No. 5212286.	1.48e+02	
14	41	100.0	25	4	5212286-32	Patent No. 5212286.	1.48e+02	
15	41	100.0	25	4	5212286-33	Patent No. 5212286.	1.48e+02	
16	41	100.0	25	4	5212286-36	Patent No. 5212286.	1.48e+02	
17	41	100.0	25	4	5212286-31	Patent No. 5212286.	1.48e+02	
18	41	100.0	25	4	5202239-16	Patent No. 5202239.	1.48e+02	
19	41	100.0	25	4	5212286-27	Patent No. 5212286.	1.48e+02	
20	41	100.0	25	4	5212286-25	Patent No. 5212286.	1.48e+02	
21	41	100.0	25	4	5212286-34	Patent No. 5212286.	1.48e+02	
22	41	100.0	25	4	5212286-35	Patent No. 5212286.	1.48e+02	
23	41	100.0	27	4	5204327-2	Patent No. 5204327.	1.48e+02	

ALIGNMENTS

[illegible]

Seq. Secar. Similarity 100.0%; Rec. NO. 1.46e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

CC Patent No. 5434133
CC GENERAL INFORMATION:
CC APPLICANT: TANAKA, SHOJI
CC APPLICANT: MINAMITAKE, YOSHIHARU
CC APPLICANT: KITAJIMA, YASUO
CC APPLICANT: FURUYA, MAYUMI
CC APPLICANT: MATSUO, HISAYUKI
CC TITLE OF INVENTION: CNP ANALOG PEPTIDES AND THEIR USE
CC NUMBER OF SEQUENCES: 42
CC CORRESPONDENCE ADDRESS:
CC ADDRESSEE: CUSHMAN, DARBY & CUSHMAN
CC STREET: 1625 L STREET, N.W.
CC CITY: WASHINGTON
CC STATE: D.C.
CC COUNTRY: USA
CC ZIP: 20036
CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: Floppy disk
CC COMPUTER: IBM PC compatible
CC OPERATING SYSTEM: PC-DOS/MS-DOS
CC SOFTWARE: Patentin Release #1.0, Version #1.25
CC CURRENT APPLICATION NUMBER: US/07/828,450
CC FILING DATE: 19920131
CC CLASSIFICATION: 530
CC ATTORNEY/AGENT INFORMATION:
CC NAME: SCOTT, WATSON T.
CC REGISTRATION NUMBER: 26,581
CC REFERENCE/DOCKET NUMBER: 9437/94133
CC TELECOMMUNICATION INFORMATION:
CC TELEPHONE: 202-861-3067
CC TELEFAX: 202-822-0944
CC TELEX: 6714627 CUSH
CC INFORMATION FOR SEQ ID NO: 26:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 22 amino acids
CC TYPE: AMINO ACID
CC STRANDEDNESS: single
CC TOPOLOGY: linear
CC MOLECULE TYPE: peptide
CC SEQUENCE 22 AA: 2369 MW; 2338 CN;
CC
CC Query Match 100.0%; Score 41; DB 1; Length 22;
CC Best Local Similarity 100.0%; Pred. No. 1.48e+02;
CC Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
CC
CC Db 18 NSFRY 22
CC 11111
CC Qy 1 NSFRY 5
CC
CC RESULT 3
CC ID US-07-828-450-27 STANDARD; PRT; 22 AA.
CC AC xxxxxx
CC DT 01-JAN-1900
CC DE Patent No. 5212286.
CC XX Patent No. 5212286
CC CC APPLICANT: LEWICKI, JOHN A.; SCARBOROUGH, ROBERT M.
CC CC TITLE OF INVENTION: ATRIAL NATRIURETIC/VASODILATOR
CC CC PEPTIDE COMPOUNDS
CC CC NUMBER OF SEQUENCES: 68
CC CC CURRENT APPLICATION DATA:
CC CC APPLICATION NUMBER: US/07/870,795
CC CC FILING DATE: 05-JUN-1986
CC CC PRIOR APPLICATION DATA:
CC CC APPLICATION NUMBER: 766,030
CC CC FILING DATE: 08-MAY-1985
CC CC APPLICATION NUMBER: 602,117
CC CC FILING DATE: 09-APR-1984
CC CC APPLICATION NUMBER: 616,488
CC CC FILING DATE: 01-JUN-1984
CC CC SEQ ID NO: 48
CC CC LENGTH: 23
CC CC SEQUENCE 25 AA: 2740 MW; 3445 CN;
CC
CC Query Match 100.0%; Score 41; DB 4; Length 23;
CC Best Local Similarity 100.0%; Pred. No. 1.48e+02;
CC Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
CC
CC Db 19 NSFRY 23
CC 11111

CC CITY: WASHINGTON
CC STATE: D.C.
CC COUNTRY: USA
CC ZIP: 20036
CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: Floppy disk
CC COMPUTER: IBM PC compatible
CC OPERATING SYSTEM: PC-DOS/MS-DOS
CC SOFTWARE: Patentin Release #1.0, Version #1.25
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: US/07/828,450
CC FILING DATE: 19920131
CC CLASSIFICATION: 530
CC ATTORNEY/AGENT INFORMATION:
CC NAME: SCOTT, WATSON T.
CC REGISTRATION NUMBER: 26,581
CC REFERENCE/DOCKET NUMBER: 9437/94133
CC TELECOMMUNICATION INFORMATION:
CC TELEPHONE: 202-861-3067
CC TELEFAX: 202-822-0944
CC TELEX: 6714627 CUSH
CC INFORMATION FOR SEQ ID NO: 27:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 22 amino acids
CC TYPE: AMINO ACID
CC STRANDEDNESS: single
CC TOPOLOGY: linear
CC MOLECULE TYPE: peptide
CC SEQUENCE 22 AA: 2369 MW; 2338 CN;
CC
CC Query Match 100.0%; Score 41; DB 1; Length 22;
CC Best Local Similarity 100.0%; Pred. No. 1.48e+02;
CC Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
CC
CC Db 18 NSFRY 22
CC 11111
CC Qy 1 NSFRY 5
CC
CC RESULT 4
CC ID 5212286-48 STANDARD; PRT; 25 AA.
CC AC xxxxxx
CC DT 01-JAN-1900
CC DE Patent No. 5212286.
CC XX Patent No. 5212286
CC CC APPLICANT: LEWICKI, JOHN A.; SCARBOROUGH, ROBERT M.
CC CC TITLE OF INVENTION: ATRIAL NATRIURETIC/VASODILATOR
CC CC PEPTIDE COMPOUNDS
CC CC NUMBER OF SEQUENCES: 68
CC CC CURRENT APPLICATION DATA:
CC CC APPLICATION NUMBER: US/07/870,795
CC CC FILING DATE: 05-JUN-1986
CC CC PRIOR APPLICATION DATA:
CC CC APPLICATION NUMBER: 766,030
CC CC FILING DATE: 08-MAY-1985
CC CC APPLICATION NUMBER: 602,117
CC CC FILING DATE: 09-APR-1984
CC CC APPLICATION NUMBER: 616,488
CC CC FILING DATE: 01-JUN-1984
CC CC SEQ ID NO: 48
CC CC LENGTH: 23
CC CC SEQUENCE 25 AA: 2740 MW; 3445 CN;
CC
CC Query Match 100.0%; Score 41; DB 4; Length 23;
CC Best Local Similarity 100.0%; Pred. No. 1.48e+02;
CC Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
CC
CC Db 19 NSFRY 23
CC 11111

Qy 1 NSFry 5

RESULT 5

ID 5212286-47 STANDARD: PRT: 25 AA.
XX xxxxxx
XX 01-JAN-1900
XX Patent No. 5212286.
XX Patent No. 5212286
CC APPLICANT: LEWICKI, JOHN A.; SCARBOROUGH, ROBERT M.
CC TITLE OF INVENTION: ATRIAL NATRIURETIC/VASODILATOR
CC PEPTIDE COMPOUNDS
CC NUMBER OF SEQUENCES: 68
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: US/07/870,795
CC FILING DATE: 05-JUN-1986
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: 766,030
CC FILING DATE: 08-MAY-1985
CC APPLICATION NUMBER: 602,117
CC FILING DATE: 09-APR-1984
CC APPLICATION NUMBER: 616,488
CC FILING DATE: 01-JUN-1984
CC SEQ ID NO:47:
CC LENGTH: 23
SQ SEQUENCE 25 AA; 2768 MW; 3310 CN;

Query Match 100.0%; Score 41; DB 4; Length 23;
Best Local Similarity 100.0%; Pred. No. 1.48e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 19 NSFry 23

Qy 1 NSFry 5

RESULT 6

ID 5212286-39 STANDARD: PRT: 25 AA.
XX xxxxxx
XX 01-JAN-1900
XX Patent No. 5212286.
XX Patent No. 5212286
CC APPLICANT: LEWICKI, JOHN A.; SCARBOROUGH, ROBERT M.
CC TITLE OF INVENTION: ATRIAL NATRIURETIC/VASODILATOR
CC PEPTIDE COMPOUNDS
CC NUMBER OF SEQUENCES: 68
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: US/07/870,795
CC FILING DATE: 05-JUN-1986
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: 766,030
CC FILING DATE: 08-MAY-1985
CC APPLICATION NUMBER: 602,117
CC FILING DATE: 09-APR-1984
CC APPLICATION NUMBER: 616,488
CC FILING DATE: 01-JUN-1984
CC SEQ ID NO:39:
CC LENGTH: 23
SQ SEQUENCE 25 AA; 2772 MW; 3366 CN;

Query Match 100.0%; Score 41; DB 4; Length 23;
Best Local Similarity 100.0%; Pred. No. 1.48e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 19 NSFry 23

Qy 1 NSFry 5

RESULT 7
ID 5212286-37 STANDARD: PRT: 25 AA.
XX xxxxxx
XX 01-JAN-1900
XX Patent No. 5212286.
XX Patent No. 5212286
CC APPLICANT: LEWICKI, JOHN A.; SCARBOROUGH, ROBERT M.
CC TITLE OF INVENTION: ATRIAL NATRIURETIC/VASODILATOR
CC PEPTIDE COMPOUNDS
CC NUMBER OF SEQUENCES: 68
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: US/07/870,795
CC FILING DATE: 05-JUN-1986
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: 766,030
CC FILING DATE: 08-MAY-1985
CC APPLICATION NUMBER: 602,117
CC FILING DATE: 09-APR-1984
CC APPLICATION NUMBER: 616,488
CC FILING DATE: 01-JUN-1984
CC SEQ ID NO:37:
CC LENGTH: 23
SQ SEQUENCE 25 AA; 2754 MW; 3345 CN;

Query Match 100.0%; Score 41; DB 4; Length 23;
Best Local Similarity 100.0%; Pred. No. 1.48e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 19 NSFry 23

Qy 1 NSFry 5

RESULT 8

ID 5212286-43 STANDARD: PRT: 25 AA.
XX xxxxxx
XX 01-JAN-1900
XX Patent No. 5212286.
XX Patent No. 5212286
CC APPLICANT: LEWICKI, JOHN A.; SCARBOROUGH, ROBERT M.
CC TITLE OF INVENTION: ATRIAL NATRIURETIC/VASODILATOR
CC PEPTIDE COMPOUNDS
CC NUMBER OF SEQUENCES: 68
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: US/07/870,795
CC FILING DATE: 05-JUN-1986
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: 766,030
CC FILING DATE: 08-MAY-1985
CC APPLICATION NUMBER: 602,117
CC FILING DATE: 09-APR-1984
CC APPLICATION NUMBER: 616,488
CC FILING DATE: 01-JUN-1984
CC SEQ ID NO:43:
CC LENGTH: 23
SQ SEQUENCE 25 AA; 2768 MW; 3233 CN;

Query Match 100.0%; Score 41; DB 4; Length 23;
Best Local Similarity 100.0%; Pred. No. 1.48e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 19 NSFRY 23
QY 1 NSFRY 5

RESULT 9
ID 5212286-45 STANDARD; PRT: 25 AA.
XX
AC
XX
XX
DT 01-JAN-1900
XX
DE Patent No. 5212286.
XX
XX Patent No. 5212286
CC APPLICANT: LEWICKI, JOHN A.; SCARBOROUGH, ROBERT M.
CC TITLE OF INVENTION: ATRIAL NATRIURETIC/VASODILATOR
CC PEPTIDE COMPOUNDS
CC NUMBER OF SEQUENCES: 68
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: US/07/870,795
CC FILING DATE: 05-JUN-1986
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: 766,030
CC FILING DATE: 08-MAY-1985
CC APPLICATION NUMBER: 602,117
CC FILING DATE: 09-APR-1984
CC APPLICATION NUMBER: 616,488
CC FILING DATE: 01-JUN-1984
CC SEQ ID NO:45:
CC LENGTH: 23
CC SEQUENCE 25 AA: 2768 MW; 3317 CN;
SQ

Query Match 100.0%; Score 41; DB 4; Length 23;
Best Local Similarity 100.0%; Pred. No. 1.48e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 19 NSFRY 23
QY 1 NSFRY 5

RESULT 10
ID 5212286-44 STANDARD; PRT: 25 AA.
XX
AC
XX
XX
DT 01-JAN-1900
XX
DE Patent No. 5212286.
XX
XX Patent No. 5212286
CC APPLICANT: LEWICKI, JOHN A.; SCARBOROUGH, ROBERT M.
CC TITLE OF INVENTION: ATRIAL NATRIURETIC/VASODILATOR
CC PEPTIDE COMPOUNDS
CC NUMBER OF SEQUENCES: 68
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: US/07/870,795
CC FILING DATE: 05-JUN-1986
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: 766,030
CC FILING DATE: 08-MAY-1985
CC APPLICATION NUMBER: 602,117
CC FILING DATE: 09-APR-1984
CC APPLICATION NUMBER: 616,488
CC FILING DATE: 01-JUN-1984
CC SEQ ID NO:44:
CC LENGTH: 23
CC SEQUENCE 25 AA: 2768 MW; 3261 CN;
SQ

Query Match 100.0%; Score 41; DB 4; Length 23;
Best Local Similarity 100.0%; Pred. No. 1.48e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 19 NSFRY 23
QY 1 NSFRY 5

RESULT 11
ID US-08-257-446-5 STANDARD; PRT: 24 AA.
XX
AC
XX
XX
DT
XX
DE
XX
XX Sequence 5, Application US/08257446
XX
XX Sequence 5, Application US/08257446
CC Patent No. 5565606
CC GENERAL INFORMATION:
CC APPLICANT: Briephol, Gerhard
CC APPLICANT: Knolle, Jochen
CC TITLE OF INVENTION: The Synthesis of Peptide
CC TITLE OF INVENTION: Aminoalkylamides and Peptide Hydrazides by the Solid Ph
CC TITLE OF INVENTION: Method
CC NUMBER OF SEQUENCES: 6
CC CORRESPONDENCE ADDRESS:
CC ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &
CC ADDRESSEE: Dunner
CC STREET: 1300 I Street, N.W., Suite 700
CC CITY: Washington
CC STATE: D.C.
CC ZIP: 20005-3315
CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: Floppy disk
CC COMPUTER: IBM PC Compatible
CC OPERATING SYSTEM: PC-DOS/MS-DOS
CC SOFTWARE: Patent In Release #1.0, Version #1.25
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: US/08/257,446
CC FILING DATE:
CC CLASSIFICATION: 530
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 783,335
CC FILING DATE: 28-OCT-1991
CC ATTORNEY/AGENT INFORMATION:
CC NAME: Lindeman, Jeffrey A.
CC REGISTRATION NUMBER: 34,658
CC REFERENCE/DOCKET NUMBER: 02481-0503-01000
CC TELECOMMUNICATION INFORMATION:
CC TELEPHONE: 202-208-4000
CC TELEFAX: 202-408-4400
CC INFORMATION FOR SEQ ID NO: 5:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 24 amino acids
CC TYPE: amino acid
CC STRANDEDNESS: single
CC TOPOLOGY: linear
CC MOLECULE TYPE: peptide
SQ SEQUENCE 24 AA: 2552 MW; 2660 CN;

Query Match 100.0%; Score 41; DB 1; Length 24;
Best Local Similarity 100.0%; Pred. No. 1.48e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 20 NSFRY 24
QY 1 NSFRY 5

RESULT 12
ID 5212286-55 STANDARD; PRT: 27 AA.
XX
AC
XX
XX
DT 01-JAN-1900

XX DE Patent No. 5212286.
XX DE Patent No. 5212286.
CC APPLICANT: LEWICKI, JOHN A.; SCARBOROUGH, ROBERT M.
CC TITLE OF INVENTION: ATRIAL NATRIURETIC/VASODILATOR
CC PEPTIDE COMPOUNDS
CC NUMBER OF SEQUENCES: 68
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: US/07/870,795
CC FILING DATE: 05-JUN-1986
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: 766,030
CC FILING DATE: 08-MAY-1985
CC APPLICATION NUMBER: 602,117
CC FILING DATE: 09-APR-1984
CC APPLICATION NUMBER: 616,488
CC FILING DATE: 01-JUN-1984
CC SEQ ID NO:55;
CC LENGTH: 25
CC SEQUENCE 27 AA; 2960 MW; 3801 CN;

Query Match 100.0%; Score 41; DB 4; Length 25;
Best Local Similarity 100.0%; Pred. No. 1.48e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 21 NSFRY 25
|||||
QY 1 NSFRY 5

RESULT 13
ID 5212286-49 STANDARD; PRT; 27 AA.
XX AC xxxxxx
XX DT 01-JAN-1900
XX DE Patent No. 5212286.
XX DE Patent No. 5212286
CC APPLICANT: LEWICKI, JOHN A.; SCARBOROUGH, ROBERT M.
CC TITLE OF INVENTION: ATRIAL NATRIURETIC/VASODILATOR
CC PEPTIDE COMPOUNDS
CC NUMBER OF SEQUENCES: 68
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: US/07/870,795
CC FILING DATE: 05-JUN-1986
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: 766,030
CC FILING DATE: 08-MAY-1985
CC APPLICATION NUMBER: 602,117
CC FILING DATE: 09-APR-1984
CC APPLICATION NUMBER: 616,488
CC FILING DATE: 01-JUN-1984
CC SEQ ID NO:49;
CC LENGTH: 25
CC SEQUENCE 27 AA; 3001 MW; 3736 CN;

Query Match 100.0%; Score 41; DB 4; Length 25;
Best Local Similarity 100.0%; Pred. No. 1.48e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 21 NSFRY 25
|||||
QY 1 NSFRY 5

RESULT 14
ID 5212286-32 STANDARD; PRT; 27 AA.
XX AC xxxxxx
XX AC xxxxxx

DT 01-JAN-1900
XX DE Patent No. 5212286.
XX DE Patent No. 5212286
CC APPLICANT: LEWICKI, JOHN A.; SCARBOROUGH, ROBERT M.
CC TITLE OF INVENTION: ATRIAL NATRIURETIC/VASODILATOR
CC PEPTIDE COMPOUNDS
CC NUMBER OF SEQUENCES: 68
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: US/07/870,795
CC FILING DATE: 05-JUN-1986
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: 766,030
CC FILING DATE: 08-MAY-1985
CC APPLICATION NUMBER: 602,117
CC FILING DATE: 09-APR-1984
CC APPLICATION NUMBER: 616,488
CC FILING DATE: 01-JUN-1984
CC SEQ ID NO:32;
CC LENGTH: 25
CC SEQUENCE 27 AA; 2942 MW; 3718 CN;

Query Match 100.0%; Score 41; DB 4; Length 25;
Best Local Similarity 100.0%; Pred. No. 1.48e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 21 NSFRY 25
|||||
QY 1 NSFRY 5

RESULT 15
ID 5212286-33 STANDARD; PRT; 27 AA.
XX AC xxxxxx
XX DT 01-JAN-1900
XX DE Patent No. 5212286.
XX DE Patent No. 5212286
CC APPLICANT: LEWICKI, JOHN A.; SCARBOROUGH, ROBERT M.
CC TITLE OF INVENTION: ATRIAL NATRIURETIC/VASODILATOR
CC PEPTIDE COMPOUNDS
CC NUMBER OF SEQUENCES: 68
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: US/07/870,795
CC FILING DATE: 05-JUN-1986
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: 766,030
CC FILING DATE: 08-MAY-1985
CC APPLICATION NUMBER: 602,117
CC FILING DATE: 09-APR-1984
CC APPLICATION NUMBER: 616,488
CC FILING DATE: 01-JUN-1984
CC SEQ ID NO:33;
CC LENGTH: 25
CC SEQUENCE 27 AA; 2942 MW; 3774 CN;

Query Match 100.0%; Score 41; DB 4; Length 25;
Best Local Similarity 100.0%; Pred. No. 1.48e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 21 NSFRY 25
|||||
QY 1 NSFRY 5

Search completed: Wed Jun 16 13:25:06 1999
Job time : 6 secs.

WQESREH

(TM)

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MPsrch_pp protein - protein database search, using Smith-Waterman algorithm

Run on: Wed Jun 16 13:23:15 1999; MasPar time 2.89 Seconds
69.204 Million cell updates/sec
Tubular output not generated.

Title: >US-09-027-777B-3
Description: (1-5) from US0902777B.pap
Perfect Score: 41
Sequence: 1 NSFRY 5

Scoring table: PAM 150
Gap 15

Searched: 122810 seqs, 40068593 residues

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database: pir60
1:pir1 2:pir2 3:pir3 4:pir4

Statistics: Mean 20.516; Variance 23.884; scale 0.859

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description	Pred. No.
1	41	100.0	110	2	C71160	hypothetical protein
2	41	100.0	128	2	S14872	atrial natriuretic pe
3	41	100.0	137	2	S55915	ribosomal protein L28
4	41	100.0	137	1	R5RT28	ribosomal protein L28
5	41	100.0	137	2	I48738	ribosomal protein L28
6	41	100.0	149	1	AWDC	atrial natriuretic pe
7	41	100.0	150	1	S13107	atrial natriuretic pe
8	41	100.0	151	1	AWHU	natriuretic peptide A
9	41	100.0	152	1	AWRT	atrial natriuretic fa
10	41	100.0	152	1	AWBO	atrial natriuretic pe
11	41	100.0	152	1	AWMS	atrial natriuretic pe
12	41	100.0	153	2	S14873	atrial natriuretic pe
13	41	100.0	153	1	AWRB	atrial natriuretic pe
14	41	100.0	161	4	I55480	hypothetical natriure
15	41	100.0	635	2	T00602	hypothetical protein
16	41	100.0	740	2	JC6010	formate C-acetyltrans
17	41	100.0	746	2	G65100	formate C-acetyltrans
18	39	95.1	102	2	T02917	hypothetical protein
19	39	95.1	107	2	E71142	hypothetical protein
20	39	95.1	230	2	F65192	hypothetical protein
21	39	95.1	240	2	H69926	ribonucleoside-diphos
22	39	95.1	310	2	G70330	ADP-L-glycero-D-manno
23	39	95.1	315	2	H64082	hypothetical protein

24	39	95.1	331	2	JC5441	cathepsin L-like cyst
25	39	95.1	331	2	JC5442	cathepsin L-like cyst
26	39	95.1	331	2	JC5443	cathepsin L-like cyst
27	39	95.1	339	2	A53810	cathepsin L (EC 3.4.2
28	39	95.1	390	2	F69086	pyruvate formate-lyase
29	39	95.1	439	2	H70582	probable transposase
30	39	95.1	455	2	E64454	proline--trna ligase
31	39	95.1	482	2	C69181	proline--trna ligase
32	39	95.1	575	2	H59450	prolyl-trna synthetas
33	39	95.1	589	2	H71153	hypothetical protein
34	39	95.1	700	2	B69667	ribonucleoside-diphos
35	39	95.1	718	2	S06068	peroxidase (EC 1.11.1
36	39	95.1	723	2	S40820	hypothetical protein
37	39	95.1	730	2	S97384	catalase (EC 1.11.1.6
38	39	95.1	745	1	ORHUM	myeloperoxidase (EC 1
39	39	95.1	786	2	A53939	kinesin homolog KRP1
40	39	95.1	825	2	C28894	myeloperoxidase (EC 1
41	39	95.1	830	2	B28894	myeloperoxidase (EC 1
42	39	95.1	863	2	S74447	ferrichrome-iron rece
43	39	95.1	1065	2	I40169	carbamoyl-phosphate s
44	39	95.1	1147	2	JC5028	nitric-oxide synthase
45	38	92.7	659	2	JE0293	3',5'-cyclic-nucleoti

ALIGNMENTS

RESULT 1

ENTRY
TITLE
ORGANISM
DATE
C71160 #type complete
hypothetical protein PH0480 - Pyrococcus horikoshii
#formal_name Pyrococcus horikoshii
14-Aug-1998 #sequence_revision 14-Aug-1998 #text_change
14-Aug-1998

ACCESSIONS
REFERENCE
#authors
C71160
A71000
Kawarabayashi, Y.; Sawada, M.; Horikawa, H.; Haikawa, Y.;
Hino, Y.; Yamamoto, S.; Sekine, M.; Baba, S.; Kosugi, H.;
Hosoyama, A.; Nagai, Y.; Sakai, M.; Ogura, K.; Otsuka, R.;
Nakazawa, H.; Takamiya, M.; Ohfuku, Y.; Funahashi, T.;
Tanaka, T.; Kudo, Y.; Yamazaki, J.; Kishida, N.; Oguchi,
A.; Aoki, K.; Yoshizawa, T.; Nakamura, Y.; Robb, F.T.;
Horikoshi, K.; Masuchi, Y.; Shizuya, H.; Kikuchi, H.

#journal
#title
DNA Res. (1998) 5:55-76
Complete sequence and gene organization of the genome of a
hyper-thermophilic archaeobacterium, Pyrococcus horikoshii
OT3.

#cross-references MUID:98344137

#accession C71160
#status preliminary; nucleic acid sequence not shown;
translation not shown
#molecule_type DNA
#residues 1110 #label KAW
#cross-references GB:AP000002; NID:g3236129; PID:d1030511; PID:g3256885
#experimental_source strain OT3
#note this accession replaces an interim accession for a
sequence replaced by GenBank

GENETICS
#gene
PH0480

SUMMARY
#length 110 #molecular-weight 12260 #checksum 6038

Query Match 100.0%; Score 41; DB 2; Length 110;

Best Local Similarity 100.0%; Pred. No. 4.81e+01;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 54 NSFRY 58

Oy 1 NSFRY 5

RESULT 2

ENTRY
TITLE
ORGANISM
DATE
S14872 #type fragment
atrial natriuretic peptide precursor - guinea pig (fragment)
#formal_name Cavia porcellus #common_name guinea pig
20-Feb-1995 #sequence_revision 30-Jan-1998 #text_change

```

#accession S13072
##molecule_type mRNA
##residues 1-137 ##label WOO
##cross-references EMBL:X52619; NID:g57112; PID:g57113
#accession A30448
##molecule_type protein
##residues 2-13,65-94,109-137 ##label W02
CLASSIFICATION #superfamily rat ribosomal protein L28
KEYWORDS protein biosynthesis; ribosome
FEATURE
2-137 #product ribosomal protein L28 #status experimental
#label MAT
SUMMARY #length 137 #molecular-weight 15849 #checksum 7501

Query Match 100.0%; Score 41; DB 1; Length 137;
Best Local Similarity 100.0%; Pred. No. 4.81e+01;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 36 NSFRY 40
|||||
QY 1 NSFRY 5

RESULT 5
ENTRY I48738 #type complete
TITLE ribosomal protein L28 - mouse
ORGANISM #formal_name Mus musculus #common_name house mouse
DATE 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change
23-Feb-1997

ACCESSIONS I48738
REFERENCE I48738 #status preliminary; translated from GB/EMBL/DDBJ
#authors Burke, P.S.; Liim, E.; Lin, C.S.; Wolgemuth, D.J.
#journal Gene (1994) 142:315-316
#title Sequence and expression of a cDNA encoding the mouse
homologue of the rat ribosomal protein L28.
#cross-references MUID:94252590
#accession I48738
##status preliminary; translated from GB/EMBL/DDBJ
##molecule_type mRNA
##residues 1-137 ##label RES
##cross-references EMBL:X74856; NID:g488834; PID:g488835

GENETICS L28
#gene #superfamily rat ribosomal protein L28
CLASSIFICATION #length 137 #molecular-weight 15733 #checksum 6283
SUMMARY

Query Match 100.0%; Score 41; DB 2; Length 137;
Best Local Similarity 100.0%; Pred. No. 4.81e+01;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 36 NSFRY 40
|||||
QY 1 NSFRY 5

RESULT 6
ENTRY AWDC
TITLE atrial natriuretic peptide precursor - dog
ALTERNATE_NAMES ANP; atrial natriuretic polypeptide
ORGANISM #formal_name Canis lupus familiaris #common_name dog
DATE 31-Mar-1988 #sequence_revision 31-Mar-1988 #text_change
22-Jan-1999
ACCESSIONS A25302
REFERENCE A90119
#authors Oikawa, S.; Imai, M.; Inuzuka, C.; Tawaragi, Y.; Nakazato,
H.; Matsuo, H.
#journal Biochem. Biophys. Res. Commun. (1985) 132:892-899
#title Structure of dog and rabbit precursors of atrial natriuretic
polypeptides deduced from nucleotide sequence of cloned
cDNA.
#cross-references MUID:86076957
#accession A25302
##molecule_type mRNA

```



```

##residues 1-149 #label OIK
##cross-references GB:M12045; NID:gl63900; PID:gl63901
CLASSIFICATION #superfamily natriuretic peptide A precursor
KEYWORDS atrium; diuretic; hormone; natriuretic; osmoregulation
FEATURE
1-23 #domain signal sequence #status predicted #label SIG\
24-149 #product gamma atrial natriuretic factor #status
predicted #label ANF\
122-149 #product alpha atrial natriuretic peptide #status
predicted #label ANP\
128-144 #disulfide_bonds #status predicted
#length 149 #molecular_weight 15819 #checksum 8040
SUMMARY
Query Match 100.0%; Score 41; DB 1; Length 149;
Best Local Similarity 100.0%; Pred. No. 4.81e+01;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 145 NSFRY 149
QY 1 NSFRY 5
|||||

RESULT 7
ENTRY #type complete
TITLE atrial natriuretic peptide precursor - pig
CONTAINS alpha atrial natriuretic peptide; gamma atrial natriuretic
factor (cardiodilatin)
ORGANISM #formal name Sus scrofa domestica #common_name domestic pig
DATE 21-Nov-1993 #sequence_revision 14-Jul-1994 #text_change
20-Mar-1998
ACCESSIONS S13107; A60899
REFERENCE S13107
#authors Maegert, H.J.; Appelhans, H.; Gassen, H.G.; Forssmann, W.G.
#journal Nucleic Acids Res. (1990) 18:6704
#title Nucleotide sequence of a porcine prepro atrial natriuretic
peptide (ANP) cDNA.
#cross-references MUID:91067478
#accession S13107
#molecule_type mRNA
#residues 1-150 #label MAE
##cross-references EMBL:X54669; NID:gl1883; PID:gl1884
A60899
REFERENCE
#authors Forssmann, W.G.; Hock, D.; Lottspeich, A.; Henschen, A.;
Kreye, V.; Christmann, M.; Reinecke, M.; Metz, J.;
Carlquist, M.; Mutt, V.
#journal Anat. Embryol. (1983) 168:307-313
#title The right auricle of the heart is an endocrine organ.
Cardiodilatin as a peptide hormone candidate.
#accession A60899
#molecule_type protein
#residues 25-54 #label FOR
CLASSIFICATION #superfamily natriuretic peptide A precursor
KEYWORDS atrium; diuretic; hormone; natriuretic; osmoregulation
FEATURE
1-24 #domain signal sequence #status predicted #label SIG\
25-150 #product gamma atrial natriuretic factor #status
predicted #label ANF\
123-150 #product alpha atrial natriuretic peptide #status
predicted #label ANP\
129-145 #disulfide_bonds #status predicted
#length 150 #molecular_weight 16351 #checksum 9859
SUMMARY
Query Match 100.0%; Score 41; DB 1; Length 150;
Best Local Similarity 100.0%; Pred. No. 4.81e+01;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 146 NSFRY 150
QY 1 NSFRY 5
|||||

RESULT 8
ENTRY #type complete

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TITLE natriuretic peptide A precursor - human
ALTERNATE_NAMES ANF; atrial natriuretic factor; atrial natriuretic protein;
prepronatriodilatin (PND)
CONTAINS atrial alpha natriuretic peptide (ANP); cardiodilatin (atrial
gamma natriuretic factor)
ORGANISM #formal_name Homo sapiens #common_name man
DATE 15-Nov-1984 #sequence_revision 15-Nov-1984 #text_change
20-Mar-1998
ACCESSIONS A22693; B22693; A01424; B29370; A32733; I58054; S14097;
I39458; I39459; I39460; I37167
REFERENCE A22693
#authors Nemer, M.; Chamberland, M.; Sirois, D.; Argentin, S.; Drouin,
J.; Dixon, R.A.F.; Zivin, R.A.; Condra, J.H.
#journal Nature (1984) 312:654-656
#title Gene structure of human cardiac hormone precursor,
pronatriodilatin.
#cross-references MUID:85061626
#accession A22693
#molecule_type DNA
#residues 1-151 #label NEM
##cross-references GB:X01470; NID:g28687; PID:g825625
#accession E22693
#molecule_type DNA
#residues 1-151,'RR' #label NE2
##note allelic variant with UGA termination codon replaced by
CGA arginine codon
REFERENCE A01424
#authors Okawa, S.; Imai, M.; Ueno, A.; Tanaka, S.; Noguchi, T.;
Nakazato, H.; Kangawa, K.; Fukuda, A.; Matsuo, H.
#journal Nature (1984) 309:724-726
#title Cloning and sequence analysis of cDNA encoding a precursor
for human atrial natriuretic polypeptide.
#cross-references MUID:84219799
#accession A01424
#molecule_type mRNA
#residues 1-151 #label OIK
##cross-references GB:X02043; NID:g178629; PID:gl78630
A29370
REFERENCE
#authors Seidman, C.E.; Bloch, K.D.; Klein, K.A.; Smith, J.A.;
Seidman, J.G.
#journal Science (1984) 226:1206-1209
#title Nucleotide sequences of the human and mouse atrial
natriuretic factor genes.
#cross-references MUID:85065766
#accession B29370
#molecule_type DNA
#residues 1-64,'D',66-151 #label SEI
##cross-references GB:X02043
REFERENCE A32733
#authors Kangawa, K.; Matsuo, H.
#journal Biochem. Biophys. Res. Commun. (1984) 118:131-139
#title Purification and complete amino acid sequence of alpha-human
atrial natriuretic polypeptide (alpha-hANP).
#cross-references MUID:84128019
#accession A32733
#molecule_type protein
#residues 124-151 #label KAN
REFERENCE I58054
#authors Nakayama, K.; Ohkubo, H.; Hirose, T.; Inayama, S.; Nakanishi,
S.
#journal Nature (1984) 310:699-701
#title mRNA sequence for human cardiodilatin-atrial natriuretic
factor precursor and regulation of precursor mRNA in rat
atria.
#cross-references MUID:84295577
#accession I58054
#status translated from GB/EMBL/DBJ
#molecule_type mRNA
#residues 1-151 #label RES
##cross-references GB:M30262; NID:gl80181; PID:gl80182
S14097
REFERENCE
#authors Vanneste, Y.; Michel, A.; Deschodt-Lanckman, M.
#journal Eur. J. Biochem. (1991) 196:281-286

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#title      Hydrolysis of intact and Cys-Phe-cleaved human atrial
#cross-references MUID:91176998
#accession   S14097
#molecule_type protein
#residues    124-151
#note        natural and synthetic peptide subjected to kallikrein
              proteolysis

REFERENCE
#authors     Zivin, R.A.; Condra, J.H.; Dixon, R.A.; Seidah, N.G.;
              Chretien, M.; Nemer, M.; Chamberland, M.; Drouin, J.
#journal     Proc. Natl. Acad. Sci. U.S.A. (1984) 81:6325-6329
#title       Molecular cloning and characterization of DNA sequences
              encoding rat and human atrial natriuretic factors.
#cross-references MUID:85038509
#accession   I39458
#status      preliminary; translated from GB/EMBL/DBJ
#molecule_type mRNA
#residues    119-151, 'RR' #label RE2
#cross-references GB:K02044; NID:g178631; PID:g178632
REFERENCE
#authors     Maki, M.; Parmentier, M.; Inagami, T.
#journal     J. Biol. Chem. (1985) 260:4568-4571
#title       The gene for rat atrial natriuretic factor.
#cross-references MUID:85182558
#accession   A22570
#molecule_type DNA
#residues    1-152 #label ARG
#cross-references GB:K02062; NID:g202899; PID:g202900
REFERENCE
#authors     Yamanaka, M.; Greenberg, B.; Johnson, L.; Seilhamer, J.;
              Brewer, M.; Friedemann, T.; Miller, J.; Atlas, S.; Laragh,
              J.; Lewicki, J.; Fiddes, J.
#journal     Nature (1984) 309:719-722
#title       Cloning and sequence analysis of the cDNA for the rat atrial
              natriuretic factor precursor.
#cross-references MUID:84219797
#accession   A01425
#molecule_type mRNA
#residues    1-152 #label YAM
#cross-references EMBL:X00665; NID:g55711; PID:g55712
REFERENCE
#authors     Maki, M.; Takayanagi, R.; Misono, K.S.; Pandey, K.N.;
              Tibbatts, C.; Inagami, T.
#journal     Nature (1984) 309:722-724
#title       Structure of rat atrial natriuretic factor precursor deduced
              from cDNA sequence.
#cross-references MUID:84219798
#accession   A93332
#molecule_type mRNA
#residues    1-152 #label MAK
#cross-references GB:X00665; EMBL:X00658; NID:g55711; PID:g55712
REFERENCE
#authors     Seidman, C.E.; Duby, A.D.; Choi, E.; Graham, R.M.; Haber, E.;
              Homcy, C.; Smith, J.A.; Seidman, J.G.
#journal     Science (1984) 225:324-326
#title       The structure of rat preproatrial natriuretic factor as
              defined by a complementary DNA clone.
#cross-references MUID:84250178
#accession   A43617
#molecule_type mRNA
#residues    1-152 #label SEI
#cross-references GB:K02062; GB:K02063; NID:g202899; PID:g202900
REFERENCE
#authors     Atlas, S.A.; Kleinert, H.D.; Camargo, M.J.; Januszewicz, A.;
              Sealey, J.E.; Laragh, J.H.; Schilling, J.W.; Lewicki, J.A.;
              Johnson, L.K.; Maack, T.
#journal     Nature (1984) 309:717-719
#title       Purification, sequencing and synthesis of natriuretic and
              vasoactive rat atrial peptide.
#cross-references MUID:84219796
#accession   A93330
#molecule_type protein
#residues    126-149 #label ATL
REFERENCE
#accession   A94275

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Db      147 NSFRY 151
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Oy      1 NSFRY 5

RESULT      9
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TITLE       atrial natriuretic factor precursor - rat
CONTAINS    ANF(1-33); ANF(2-33); ANF(3-33); ANF(8-33); atrial
              natriuretic peptide; atriopeptin I; atriopeptin II;
              auriculin A; auriculin B; preprocardionatriin
ORGANISM    #formal name Rattus norvegicus #common_name Norway rat
DATE        19-Feb-1984 #sequence_revision 15-Nov-1984 #text_change
              26-Feb-1999
ACCESSIONS  A22570; A01425; A93332; A43617; A93330; A94275; PT0061;
              A20973; A44190; A60390; I59094; I58057; I52678
REFERENCE
#authors     Argentin, S.; Nemer, M.; Drouin, J.; Scott, G.K.; Kennedy,
              B.P.; Davies, P.L.
#journal     J. Biol. Chem. (1985) 260:4568-4571
#title       The gene for rat atrial natriuretic factor.
#cross-references MUID:85182558
#accession   A22570
#molecule_type DNA
#residues    1-152 #label ARG
#cross-references GB:K02062; NID:g202899; PID:g202900
REFERENCE
#authors     Yamanaka, M.; Greenberg, B.; Johnson, L.; Seilhamer, J.;
              Brewer, M.; Friedemann, T.; Miller, J.; Atlas, S.; Laragh,
              J.; Lewicki, J.; Fiddes, J.
#journal     Nature (1984) 309:719-722
#title       Cloning and sequence analysis of the cDNA for the rat atrial
              natriuretic factor precursor.
#cross-references MUID:84219797
#accession   A01425
#molecule_type mRNA
#residues    1-152 #label YAM
#cross-references EMBL:X00665; NID:g55711; PID:g55712
REFERENCE
#authors     Maki, M.; Takayanagi, R.; Misono, K.S.; Pandey, K.N.;
              Tibbatts, C.; Inagami, T.
#journal     Nature (1984) 309:722-724
#title       Structure of rat atrial natriuretic factor precursor deduced
              from cDNA sequence.
#cross-references MUID:84219798
#accession   A93332
#molecule_type mRNA
#residues    1-152 #label MAK
#cross-references GB:X00665; EMBL:X00658; NID:g55711; PID:g55712
REFERENCE
#authors     Seidman, C.E.; Duby, A.D.; Choi, E.; Graham, R.M.; Haber, E.;
              Homcy, C.; Smith, J.A.; Seidman, J.G.
#journal     Science (1984) 225:324-326
#title       The structure of rat preproatrial natriuretic factor as
              defined by a complementary DNA clone.
#cross-references MUID:84250178
#accession   A43617
#molecule_type mRNA
#residues    1-152 #label SEI
#cross-references GB:K02062; GB:K02063; NID:g202899; PID:g202900
REFERENCE
#authors     Atlas, S.A.; Kleinert, H.D.; Camargo, M.J.; Januszewicz, A.;
              Sealey, J.E.; Laragh, J.H.; Schilling, J.W.; Lewicki, J.A.;
              Johnson, L.K.; Maack, T.
#journal     Nature (1984) 309:717-719
#title       Purification, sequencing and synthesis of natriuretic and
              vasoactive rat atrial peptide.
#cross-references MUID:84219796
#accession   A93330
#molecule_type protein
#residues    126-149 #label ATL
REFERENCE
#accession   A94275

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Query Match      100.0%; Score 41; DB 1; Length 151;
Best Local Similarity 100.0%; Pred. No. 4.81e+01;
Matches          5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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#authors Currie, M.G.; Geller, D.M.; Cole, B.R.; Siegel, N.R.; Fox,
K.F.; Adams, S.P.; Eubanks, S.R.; Galluppi, G.R.;
Needleman, P.
#journal Science (1984) 223:67-69
#title Purification and sequence analysis of bioactive atrial
peptides (atriopectins).
#cross-references MUID:84097513
#accession A94275
##molecule_type protein
##residues 127-149 ##label CUR
REFERENCE
#authors Thibault, G.; Murthy, K.K.; Gutkowska, J.; Seldah, N.G.;
Lazure, C.; Chretien, M.; Cantin, M.
#journal Peptides (1988) 9:47-53
#title NH2-terminal fragment of rat pro-atrial natriuretic factor in
the circulation: identification, radioimmunoassay and
half-life.
#cross-references MUID:88203350
#accession PT0061
##molecule_type protein
##residues 25-28,'X',30-31,'X',33,'X',35-38 ##label THI
REFERENCE
#authors Seldah, N.G.; Lazure, C.; Chretien, M.; Thibault, G.; Garcia,
R.; Cantin, M.; Genest, J.; Nutt, R.F.; Brady, S.F.; Lyle,
T.A.; Paleveda, W.J.; Colton, C.D.; Ciccarone, T.M.; Veber,
D.F.
#journal Proc. Natl. Acad. Sci. U.S.A. (1984) 81:2640-2644
#title Amino acid sequence of homologous rat atrial peptides:
natriuretic activity of native and synthetic forms.
#cross-references MUID:84194062
#accession A20973
##molecule_type protein
##residues 118-150 ##label SE2
REFERENCE
#authors Flynn, T.G.; Davies, P.L.; Kennedy, B.P.; de Bold, M.L.; de
Bold, A.J.
#journal Science (1985) 228:323-325
#title Alignment of rat cardionatrin sequences with the
preprocardionatrin sequence from complementary DNA.
#cross-references MUID:85168263
#accession A44190
##molecule_type mRNA
##residues 1-152 ##label FLY
#cross-references GB:K02062; NID:g202899; PID:g202900
##note part of this sequence, including the amino ends of three
mature peptides, was confirmed by protein sequencing
REFERENCE
#authors Belcourt, D.; Varma, D.R.; Toney, K.; Bennett, H.P.J.
#journal Protein Expr. Purif. (1990) 1:28-32
#title Purification of rat pro-atrial natriuretic factor: a
simplified scheme using reversed-phase high-performance
liquid chromatography.
#cross-references MUID:93044510
#accession A60390
##molecule_type protein
##residues 25-39 ##label BEL
REFERENCE
#authors Gardner, D.G.; Vlasuk, G.P.; Baxter, J.D.; Fiddes, J.C.;
Lewicki, J.A.
#journal Proc. Natl. Acad. Sci. U.S.A. (1987) 84:2175-2179
#title Identification of atrial natriuretic factor gene transcripts
in the central nervous system of the rat.
#cross-references MUID:87175636
#accession I59094
##status translated from GB/EMBL/DBJ
##molecule_type mRNA
##residues 38-152 ##label RES
#cross-references GB:M15868; NID:g202903; PID:g202904
REFERENCE
#authors Kangawa, K.; Tawaragi, Y.; Oikawa, S.; Mizuno, A.;
Sakuragawa, Y.; Nakazato, H.; Fukuda, A.; Minamino, N.;
Matsuo, H.
#journal Nature (1984) 312:152-155

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#title Identification of rat gamma atrial natriuretic polypeptide
and characterization of the cDNA encoding its precursor.
#cross-references MUID:85061500
#accession I58057
##status preliminary; translated from GB/EMBL/DBJ
##molecule_type mRNA
##residues 1-152 ##label RE2
#cross-references EMBL:X01118; NID:g55716; PID:g55717
REFERENCE
#authors Flynn, T.G.
#journal Can. J. Physiol. Pharmacol. (1987) 65:2013-2020
#title The elucidation of the structure of atrial natriuretic
factor, a new peptide hormone.
#cross-references MUID:88109092
#accession I52678
##status preliminary; translated from GB/EMBL/DBJ
##molecule_type mRNA
##residues 1-51,'X',53-85,'X',87-152 ##label RE3
#cross-references GB:M27498; NID:g202905; PID:g202906
COMMENT A disulfide bond is required for full activity of atriopectins.
COMMENT Several active peptides may be derived from the carboxyl region of
this precursor.
GENETICS
#gene ANF
#introns 40/3; 149/3
CLASSIFICATION #superfamily natriuretic peptide A precursor
KEYWORDS atrium; diuretic; hormone; natriuretic; osmoregulation
FEATURE
1-24
25-152
#domain signal sequence #status predicted #label SIG\
#product pro-atrial natriuretic factor #status
experimental #label PRO\
#product cardionatrin IV #status experimental #label
CN4\
#product cardionatrin III #status experimental #label
CN3\
#product ANF(1-33) #status experimental #label ANF1\
#product ANF(2-33) #status experimental #label ANF2\
#product ANF(3-33) #status experimental #label ANF3\
#product cardionatrin I #status experimental #label CN1\
#product ANF(8-33) #status experimental #label ANF4\
#product auriculin B #status experimental #label AUB\
#product auriculin A #status experimental #label AUA\
#product atrial natriuretic factor #status predicted
#label MAT\
#product atriopeptin I #status experimental #label AT1\
#product atriopeptin II #status experimental #label AT2\
#disulfide_bonds #status experimental
SUMMARY #length 152 #molecular_weight 16556 #checksum 7818
Query Match 100.0%; Score 41; DB 1; Length 152;
Best Local Similarity 100.0%; Pred.No. 4.81e+01;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Db 146 NSFRY 150
Oy 1 NSFRY 5
RESULT 10
ENTRY
TITLE #type complete
ALTERNATE_NAMES atrial natriuretic peptide precursor - bovine
ORGANISM ANP; atrial natriuretic polypeptide
#formal_name Bos primigenius taurus #common_name cattle
DATE 30-Jun-1989 #sequence_revision 30-Jun-1989 #text_change
20-Mar-1998
ACCESSIONS A90124; A93049; A24247; A26090
REFERENCE A90124
#authors Vlasuk, G.P.; Miller, J.; Bencen, G.H.; Lewicki, J.A.
#journal Biochem. Biophys. Res. Commun. (1986) 136:396-403
#title Structure and analysis of the bovine atrial natriuretic
peptide precursor gene.
#cross-references MUID:86215205
#accession A90124

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##molecule_type DNA
##residues
##cross-references GB:M13145; NID:g162665; PID:g162666
REFERENCE
A93049
#authors
Ong, H.; McNicoll, N.; Lazure, C.; Seidah, N.; Chretien, M.;
Cantin, M.; De Lean, A.
#journal
Life Sci. (1986) 38:1309-1315
#title
Purification and sequence determination of bovine atrial
natriuretic factor.
#cross-references MUID:86173941
#accession
A93049
##molecule_type protein
##residues
123-150 #label ONG
GENETICS
#introns
40/3; 149/3
CLASSIFICATION
#superfamily natriuretic peptide A precursor
KEYWORDS
atrium; diuretic; hormone; natriuretic; osmoregulation
FEATURE
1-24
#domain signal sequence #status predicted #label SIG\
25-152
#product gamma atrial natriuretic factor #status
predicted #label ANF\
123-150
#product alpha atrial natriuretic peptide #status
experimental #label ANP\
129-145
#disulfide_bonds #status predicted
#length 152 #molecular-weight 16518 #checksum 7552
SUMMARY
Query Match 100.0%; Score 41; DB 1; Length 152;
Best Local Similarity 100.0%; Pred. No. 4.81e+01;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Db 146 NSFRY 150
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Qy 1 NSFRY 5
RESULT 11
ENTRY
TITLE
#type complete
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ORGANISM
31-Mar-1988 #sequence_revision 31-Mar-1988 #text_change
20-Mar-1998
ACCESSIONS
A29370; B43619
REFERENCE
#authors
Seidman, J.G.
#journal
Science (1984) 226:1206-1209
#title
Nucleotide sequences of the human and mouse atrial
natriuretic factor genes.
#cross-references MUID:85065766
#accession
A29370
##molecule_type DNA
##residues
1-152 #label SEI
##cross-references GB:K02781; NID:g191937; PID:g387099
GENETICS
#introns
40/3; 149/3
CLASSIFICATION
#superfamily natriuretic peptide A precursor
KEYWORDS
atrium; diuretic; hormone; natriuretic; osmoregulation
FEATURE
1-24
#domain signal sequence #status predicted #label SIG\
25-150
#product gamma atrial natriuretic factor #status
predicted #label ANF\
123-150
#product alpha atrial natriuretic peptide #status
predicted #label ANP\
129-145
#disulfide_bonds #status predicted
#length 152 #molecular-weight 16645 #checksum 9384
SUMMARY
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Best Local Similarity 100.0%; Pred. No. 4.81e+01;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Db 146 NSFRY 150
|||||
Qy 1 NSFRY 5
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RESULT 12
ENTRY
TITLE
#type complete
#formal_name Equus caballus #common_name domestic horse
ORGANISM
20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change
08-Sep-1997
ACCESSIONS
S14873
REFERENCE
#authors
Maegert, H.J.; Hanke, M.; Schmieding, G.; Teuteberg, K.;
Schulz-Knappe, P.; Forssmann, W.G.
#submission
submitted to the EMBL Data Library, March 1991
#accession
S14873
##status
preliminary
##molecule_type mRNA
##residues
1-153 #label MAE
##cross-references EMBL:X8563; NID:g1008; PID:g1009
CLASSIFICATION
#superfamily natriuretic peptide A precursor
SUMMARY
#length 153 #molecular-weight 16825 #checksum 960
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Best Local Similarity 100.0%; Pred. No. 4.81e+01;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Db 147 NSFRY 151
|||||
Qy 1 NSFRY 5
RESULT 13
ENTRY
TITLE
#type complete
#formal_name Oryctolagus cuniculus #common_name domestic
rabbit
ORGANISM
31-Mar-1988 #sequence_revision 31-Mar-1988 #text_change
20-Mar-1998
ACCESSIONS
B25302
REFERENCE
A90119
#authors
Oikawa, S.; Imai, M.; Inuzuka, C.; Tawaragi, Y.; Nakazato,
H.; Matsuo, H.
#journal
Biochem. Biophys. Res. Commun. (1985) 132:892-899
#title
Structure of dog and rabbit precursors of atrial natriuretic
polypeptides deduced from nucleotide sequence of cloned
cDNA.
#cross-references MUID:86076957
#accession
B25302
##molecule_type mRNA
##residues
1-153 #label OIK
##cross-references GB:M12046; NID:g164770; PID:g164771
CLASSIFICATION
#superfamily natriuretic peptide A precursor
KEYWORDS
atrium; diuretic; hormone; natriuretic; osmoregulation
FEATURE
1-25
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26-151
#product gamma atrial natriuretic factor #status
predicted #label ANF\
124-151
#product alpha atrial natriuretic peptide #status
predicted #label ANP\
130-146
#disulfide_bonds #status predicted
#length 153 #molecular-weight 16843 #checksum 7650
SUMMARY
Query Match 100.0%; Score 41; DB 1; Length 153;
Best Local Similarity 100.0%; Pred. No. 4.81e+01;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Db 147 NSFRY 151
|||||
Qy 1 NSFRY 5
RESULT 14
ENTRY
TITLE
#type complete
#formal_name Mus musculus #common_name house mouse
ORGANISM
31-Mar-1988 #sequence_revision 31-Mar-1988 #text_change
20-Mar-1998
ACCESSIONS
A29370; B43619
REFERENCE
#authors
Seidman, J.G.
#journal
Science (1984) 226:1206-1209
#title
Nucleotide sequences of the human and mouse atrial
natriuretic factor genes.
#cross-references MUID:85065766
#accession
A29370
##molecule_type DNA
##residues
1-152 #label SEI
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GENETICS
#introns
40/3; 149/3
CLASSIFICATION
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KEYWORDS
atrium; diuretic; hormone; natriuretic; osmoregulation
FEATURE
1-24
#domain signal sequence #status predicted #label SIG\
25-150
#product gamma atrial natriuretic factor #status
predicted #label ANF\
123-150
#product alpha atrial natriuretic peptide #status
predicted #label ANP\
129-145
#disulfide_bonds #status predicted
#length 152 #molecular-weight 16645 #checksum 9384
SUMMARY
Query Match 100.0%; Score 41; DB 1; Length 152;
Best Local Similarity 100.0%; Pred. No. 4.81e+01;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Db 146 NSFRY 150
|||||
Qy 1 NSFRY 5
```

TITLE hypothetical natriuretic peptide/phage fr coat protein mutant
fusion protein - synthetic
ORGANISM #formal_name synthetic
#note Homo sapiens (man) and phage fr genes engineered and
expressed in Escherichia coli
DATE 02-Jul-1996 #sequence_revision 05-Sep-1996 #text_change
05-Sep-1996
ACCESSIONS 155480
REFERENCE 155480
#authors Berzins, V.; Jansone, I.; Skangals, A.; Kalnins, P.; Lliepa,
S.; Baumanis, V.
#journal J. Biotechnol. (1993) 30:231-243
#title High level expression of alpha-human atrial natriuretic
factor as a fusion polypeptide with phage fr coat protein
in Escherichia coli.
#accession 155480
##status preliminary; translated from GB/EMBL/DBJ
##molecule_type DNA
##residues 1-161 #label RES
##cross-references GB:S66567; NID:g435742; PID:g435743
KEYWORDS fusion protein
SUMMARY #length 161 #molecular-weight 17287 #checksum 337
Query Match 100.0%; Score 41; DB 4; Length 161;
Best Local Similarity 100.0%; Pred. No. 4.81e+01;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Db 157 NSFRY 161
|||||
QY 1 NSFRY 5
RESULT 15
ENTRY T00602 #type complete
TITLE hypothetical protein T8K22.8 - Arabidopsis thaliana
ORGANISM #formal_name Arabidopsis thaliana #common_name mouse-ear
cress
DATE 01-Feb-1999 #sequence_revision 01-Feb-1999 #text_change
01-Feb-1999
ACCESSIONS T00602
REFERENCE 214192
#authors Rounsley, S.D.; Lin, X.; Ketchum, K.A.; Crosby, M.L.;
Brandon, R.C.; Sykes, S.M.; Kaul, S.; Mason, T.M.;
Kerlavage, A.R.; Adams, M.D.; Somerville, C.R.; Venter,
J.C.
#submission submitted to the EMBL Data Library, June 1998
#description Arabidopsis thaliana chromosome II BAC T8K22 genomic
sequence.
#accession T00602
##status preliminary; translated from GB/EMBL/DBJ.
##molecule_type DNA
##residues 1-635 #label ROU
##cross-references EMBL:AC004136; NID:g3184270; PID:g3184278
GENETICS
#map_position II
#introns 18/3
#note T8K22.8
SUMMARY #length 635 #molecular-weight 72049 #checksum 1480
Query Match 100.0%; Score 41; DB 2; Length 635;
Best Local Similarity 100.0%; Pred. No. 4.81e+01;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Db 439 NSFRY 443
|||||
QY 1 NSFRY 5

Search completed: Wed Jun 16 13:23:28 1999
Job time : 13 secs.

W P E L H

(TM)

MPSrch_pp protein - protein database search, using Smith-Waterman algorithm
Run on: Wed Jun 16 13:23:46 1999; MasPar time 2.01 Seconds
Tabular output not generated. 70.179 Million cell updates/sec

Title: >US-09-027-777B-3
Description: (1-5) from US09027777B.pep
Perfect Score: 41
Sequence: 1 NSFRY 5
Scoring table: PAM 150
Gap 15
Searched: 77977 seqs, 28268293 residues
Post-processing: Minimum Match 0%
Listing first 45 summaries
Database: swiss-prot37
1:swissprot
Statistics: Mean 21.108; Variance 20.967; scale 1.007

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES					Pred. No.		
Result No.	Query Match	Length	ID	Description			
1	41	100.0	128	ANF_CAVPO	ATRIAL NATRIURETIC FAC	1.76e+01	
2	41	100.0	136	RL28_HUMAN	60S RIBOSOMAL PROTEIN	1.76e+01	
3	41	100.0	136	RL28_MOUSE	60S RIBOSOMAL PROTEIN	1.76e+01	
4	41	100.0	136	RL28_RAT	60S RIBOSOMAL PROTEIN	1.76e+01	
5	41	100.0	149	ANF_CANFA	ATRIAL NATRIURETIC FAC	1.76e+01	
6	41	100.0	150	ANF_PIG	ATRIAL NATRIURETIC FAC	1.76e+01	
7	41	100.0	152	ANF_MOUSE	ATRIAL NATRIURETIC FAC	1.76e+01	
8	41	100.0	152	ANF_BOVIN	ATRIAL NATRIURETIC FAC	1.76e+01	
9	41	100.0	152	ANF_RAT	ATRIAL NATRIURETIC FAC	1.76e+01	
10	41	100.0	153	ANF_RABIT	ATRIAL NATRIURETIC FAC	1.76e+01	
11	41	100.0	153	ANF_HUMAN	ATRIAL NATRIURETIC FAC	1.76e+01	
12	41	100.0	153	ANF_HORSE	ATRIAL NATRIURETIC FAC	1.76e+01	
13	41	100.0	740	PFL_CLOPA	FORMATE ACETYLTRANSFER	1.76e+01	
14	41	100.0	746	TDCE_ECOLI	KETO-ACID FORMATE ACET	1.76e+01	
15	39	95.1	102	YAC1_MAIZE	TRANSPOSABLE ELEMENT A	5.00e+01	
16	39	95.1	230	YSHA_ECOLI	HYPOTHETICAL 27.2 KD P	5.00e+01	
17	39	95.1	315	REB_HAEIN	SIGMA-E FACTOR REGULAT	5.00e+01	
18	39	95.1	455	SPY_METJA	PROLYL-TRNA SYNTHETASE	5.00e+01	
19	39	95.1	482	SPY_METTH	PROLYL-TRNA SYNTHETASE	5.00e+01	
20	39	95.1	575	SPY_ARCFU	PROLYL-TRNA SYNTHETASE	5.00e+01	
21	39	95.1	700	RIPL_BACSU	RIBONUCLEOSIDE-DIPHOS	5.00e+01	
22	39	95.1	718	PERM_MOUSE	MYELOPEROXIDASE PRECUR	5.00e+01	
23	39	95.1	730	CATR_ASPNG	CATALASE R (EC 1.11.1.	5.00e+01	

24	39	95.1	745	1	PERM_HUMAN	MYELOPEROXIDASE PRECUR	5.00e+01
25	39	95.1	786	1	FL10_CHLRE	KINESIN-LIKE PROTEIN F	5.00e+01
26	39	95.1	1085	1	CARB_BACCL	CARBAMOYL-PHOSPHATE SY	5.00e+01
27	38	92.7	233	1	HEX8_ADE12	HEXON-ASSOCIATED PROTE	8.28e+01
28	38	92.7	275	1	IAP1_NPVOP	APOTOPHOSIS INHIBITOR 1	8.28e+01
29	38	92.7	299	1	PROC_CAEEL	PUTATIVE PYROLINE-5-C	8.28e+01
30	38	92.7	345	1	RIR2_LEIAM	RIBONUCLEOSIDE-DIPHOS	8.28e+01
31	38	92.7	399	1	Y47K_BPCHP	HYPOTHETICAL 47.6 KD P	8.28e+01
32	38	92.7	409	1	NADR_SALTY	TRANSCRIPTIONAL REGULA	8.28e+01
33	38	92.7	410	1	NADR_ECOLI	TRANSCRIPTIONAL REGULA	8.28e+01
34	38	92.7	422	1	CAMA_PSEPU	PUTIDAREDOXIN REDUCTAS	8.28e+01
35	38	92.7	424	1	Y114_NPVAC	HYPOTHETICAL 49.3 KD P	8.28e+01
36	38	92.7	463	1	D5DR_FUGRU	D(5)-LIKE DOPAMINE REC	8.28e+01
37	38	92.7	478	1	INI6_HUMAN	INTERFERON-INDUCED 56	8.28e+01
38	38	92.7	813	1	VGLH_HSVMD	GLYCOPROTEIN H PRECURS	8.28e+01
39	38	92.7	1314	1	TETL_CLOTE	TETANUS TOXIN PRECURSO	8.28e+01
40	38	92.7	3124	1	CAIC_CHICK	COLLAGEN ALPHA 1(XII)	8.28e+01
41	37	90.2	553	1	ZF37_MOUSE	ZINC FINGER PROTEIN 37	1.35e+02
42	37	90.2	726	1	Z184_HUMAN	ZINC FINGER PROTEIN 18	1.35e+02
43	37	90.2	753	1	YBV2_YEAST	HYPOTHETICAL 85.5 KD P	1.35e+02
44	37	90.2	886	1	YE86_SCHPO	HYPOTHETICAL 98.3 KD P	1.35e+02
45	37	90.2	1232	1	YQO5_CAEEL	HYPOTHETICAL 134.9 KD	1.35e+02

ALIGNMENTS

RESULT 1

ID ANF_CAVPO STANDARD; PRT; 128 AA.

AC P27596;

DT 01-AUG-1992 (REL. 23, CREATED)

DT 01-AUG-1992 (REL. 23, LAST SEQUENCE UPDATE)

DT 01-OCT-1996 (REL. 34, LAST ANNOTATION UPDATE)

DE ATRIAL NATRIURETIC FACTOR PRECURSOR (ANF) (ATRIAL NATRIURETIC PEPTIDE)

DE (ANP) (PREPRONATRIODILATIN) (FRAGMENT).

GN NPFA.

OS CAVIA PORCELLUS (GUINEA PIG).

OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA;

OC RODENTIA; HYSTRICOGNATHI; CAVIIDAE; CAVIA.

RN [1]

RP SEQUENCE FROM N.A.

RC TISSUE=HEART ATRIUM;

RA MAEGERT H.J., HANKE M., SCHMEDING G., TEUTEBERG K.,

RA SCHULZ-KNAPPE P., FORSSMANN W.G.;

RL SUBMITTED (MAR-1991) TO EMBL/GENBANK/DBJ DATA BANKS.

CC -!- FUNCTION: ATRIAL NATRIURETIC FACTOR (ANF) IS A POTENT VASOACTIVE

CC SUBSTANCE SYNTHESIZED IN MAMMALIAN ATRIA AND IS THOUGHT TO PLAY A

CC KEY ROLE IN CARDIOVASCULAR HOMEOSTASIS. HAS A GMP-STIMULATING

CC ACTIVITY.

CC -!- DEVELOPMENTAL STAGE: ADULT.

CC -!- A DISULFIDE BOND IS REQUIRED FOR FULL ACTIVITY OF ATRIOPEPTINS.

CC -!- SIMILARITY: BELONGS TO THE NATRIURETIC PEPTIDES FAMILY.

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CC -----

CC EMBL; X58562; G49544; -

CC PIR; S14872; S14872

CC PROSITE; PS00263; NATRIURETIC_PEPTIDE; 1.

CC PFAM; PF00212; ANP; 1.

CC KW VASOACTIVE.

CC NON TER 1 1

CC PEPTIDE 1 30 CARDIODILATIN-RELATED PEPTIDE (CDP).

CC PEPTIDE 99 126 ATRIAL NATRIURETIC PEPTIDE, ALPHA (ANP).

CC DISULFID 105 121 BY SIMILARITY.

CC SQ SEQUENCE 128 AA; 13966 MW; 2C2F552D CRC32;

Query Match 100.0%; Score 41; DB 1; Length 128;
Best Local Similarity 100.0%; Pred. No. 1.76e+01;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 122 NSFRY 126
 |||||
 QY 1 NSFRY 5

RESULT 2

ID RL28_HUMAN STANDARD; PRT; 136 AA.
 AC P46779;
 DT 01-NOV-1995 (REL. 32, CREATED)
 DT 01-NOV-1995 (REL. 32, LAST SEQUENCE UPDATE)
 DT 01-OCT-1996 (REL. 34, LAST ANNOTATION UPDATE)
 DE 60S RIBOSOMAL PROTEIN L28.
 GN RPL28.
 OS HOMO SAPIENS (HUMAN).
 OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA;
 OC PRIMATES; CATARRHINI; HOMINIDAE; HOMO.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE-COLON;
 RX MEDLINE; 95290496.
 RA FRIGERIO J.M., DAGORN J.C., IOVANNA J.L.;
 RT "Cloning, sequencing and expression of the L5, L21, L27a, L28, S5,
 S9, S10 and S29 human ribosomal protein mRNAs."
 RL BIOCHIM. BIOPHYS. ACTA 1262:84-88(1995).
 CC -1- SIMILARITY: BELONGS TO THE L28E FAMILY OF RIBOSOMAL PROTEINS.
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 CC EMBL: U14969; G550019; -
 DR RIBOSOMAL PROTEIN.
 KW INIT_MET 0 BY SIMILARITY.
 FT SEQUENCE 136 AA; 15630 MW; 75D1B88F CRC32;
 SQ

Query Match 100.0%; Score 41; DB 1; Length 136;
 Best Local Similarity 100.0%; Pred. No. 1.76e+01;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 35 NSFRY 39
 |||||
 QY 1 NSFRY 5

RESULT 3

ID RL28_MOUSE STANDARD; PRT; 136 AA.
 AC P41105;
 DT 01-FEB-1995 (REL. 31, CREATED)
 DT 01-FEB-1995 (REL. 31, LAST SEQUENCE UPDATE)
 DT 01-NOV-1995 (REL. 32, LAST ANNOTATION UPDATE)
 DE 60S RIBOSOMAL PROTEIN L28.
 GN RPL28.
 OS MUS MUSCULUS (MOUSE).
 OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA;
 OC RODENTIA; SCIUROGNATHI; MURIDAE; MURINAE; MUS.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE-TESTIS;
 RX MEDLINE; 94252590.
 RA BURKE P.S., LIUM E., LIN C.S., WOLGEMUTH D.J.;
 RT "Sequence and expression of a cDNA encoding the mouse homologue of
 RL the rat ribosomal protein L28."
 CC -1- SIMILARITY: BELONGS TO THE L28E FAMILY OF RIBOSOMAL PROTEINS.
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 CC or send an email to license@isb-sib.ch).
 CC EMBL: X74856; G488835; -
 DR MGD; MGI:101839; RPL28.
 KW RIBOSOMAL PROTEIN.
 FT INIT_MET 0 BY SIMILARITY.
 SQ SEQUENCE 136 AA; 15602 MW; ECEC217C CRC32;
 Query Match 100.0%; Score 41; DB 1; Length 136;
 Best Local Similarity 100.0%; Pred. No. 1.76e+01;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 35 NSFRY 39
 |||||
 QY 1 NSFRY 5

RESULT 4

ID RL28_RAT STANDARD; PRT; 136 AA.
 AC P17702;
 DT 01-AUG-1990 (REL. 15, CREATED)
 DT 01-FEB-1991 (REL. 17, LAST SEQUENCE UPDATE)
 DT 01-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE)
 DE 60S RIBOSOMAL PROTEIN L28.
 GN RPL28.
 OS RATTUS NORVEGICUS (RAT).
 OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA;
 OC RODENTIA; SCIUROGNATHI; MURIDAE; MURINAE; RATTUS.
 RN [1]
 RP SEQUENCE FROM N.A.; AND PARTIAL SEQUENCE.
 RC STRAIN-SPRAGUE-DAWLEY; TISSUE=LIVER;
 RX MEDLINE; 91002678.
 RA WOOL I.G., CHAN Y.-L., PAZ V., OLIVERA J.;
 RT "The primary structure of rat ribosomal proteins: the amino acid
 RT sequences of L27a and L28 and corrections in the sequences of S4 and
 RT S12."
 RL BIOCHIM. BIOPHYS. ACTA 1050:69-73(1990).
 CC -1- SIMILARITY: BELONGS TO THE L28E FAMILY OF RIBOSOMAL PROTEINS.
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 CC EMBL: X52619; G57113; -
 DR PIR; S13072; R5RT28.
 KW RIBOSOMAL PROTEIN.
 FT INIT_MET 0
 SQ SEQUENCE 136 AA; 15717 MW; 99E77527 CRC32;
 Query Match 100.0%; Score 41; DB 1; Length 136;
 Best Local Similarity 100.0%; Pred. No. 1.76e+01;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 35 NSFRY 39
 |||||
 QY 1 NSFRY 5

RESULT 5

ID ANF_CANFA STANDARD; PRT; 149 AA.
 AC P07499;
 DT 01-APR-1988 (REL. 07, CREATED)
 DT 01-APR-1988 (REL. 07, LAST SEQUENCE UPDATE)
 DT 01-OCT-1996 (REL. 34, LAST ANNOTATION UPDATE)
 DE ATRIAL NATRIURETIC FACTOR PRECURSOR (ANF) (ATRIAL NATRIURETIC PEPTIDE)

DE (ANP) (PREPRONATRIODILATIN).
GN NPPA.
OS CANIS FAMILIARIS (DOG).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA;
CC CARNIVORA; FISSIPEDIA; CANIDAE; CANIS.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE; 86076957.
RA OIKAWA S., INAI M., INUZUKA C., TAMARAGI Y., NAKAZATO H., MATSUO H.;
RT "Structure of dog and rabbit precursors of atrial natriuretic
RT polypeptides deduced from nucleotide sequence of cloned cDNA";
RL BIOCHEM. BIOPHYS. RES. COMMUN. 132:892-899(1985).
CC -!- FUNCTION: ATRIAL NATRIURETIC FACTOR (ANF) IS A POTENT VASOACTIVE
CC SUBSTANCE SYNTHESIZED IN MAMMALIAN ATRIA AND IS THOUGHT TO PLAY A
CC KEY ROLE IN CARDIOVASCULAR HOMEOSTASIS. HAS A CGMP-STIMULATING
CC ACTIVITY.
CC -!- A DISULFIDE BOND IS REQUIRED FOR FULL ACTIVITY OF ATRIOPEPTINS.
CC -!- SIMILARITY: BELONGS TO THE NATRIURETIC PEPTIDES FAMILY.
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CC
CC EMBL; M12045; G163901;
CC PIR; A25302; AWDC.
CC PROSITE; PS00263; NATRIURETIC_PEPTIDE; 1.
CC PFAM; PF00212; ANP; 1.
CC VASOACTIVE; SIGNAL. 23
CC SIGNAL 1
CC PEPTIDE 122 149 ATRIAL NATRIURETIC PEPTIDE, ALPHA (ANP).
CC DISULFID 128 144
CC SEQUENCE 149 AA; 15819 MW; D4F3A6CF CRC32;

Query Match 100.0%; Score 41; DB 1; Length 149;
Best Local Similarity 100.0%; Pred. No. 1.76e+01;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DB 145 NSFRY 149
QY 1 NSFRY 5

RESULT 6
ID ANF_PIG STANDARD; PRT; 150 AA.
AC P24259;
DT 01-MAR-1992 (REL. 21, CREATED)
DT 01-MAR-1992 (REL. 21, LAST SEQUENCE UPDATE)
DT 01-OCT-1996 (REL. 34, LAST ANNOTATION UPDATE)
DE ATRIAL NATRIURETIC FACTOR PRECURSOR (ANF) (ATRIAL NATRIURETIC PEPTIDE)
DE (ANP) (PREPRONATRIODILATIN).
GN NPPA.
OS SUS SCROFA (PIG).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA;
CC ARTIODACTYLA; SUIFORMES; SUINA; SUIDAE; SUS.
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=HEART RIGHT ATRIUM;
RX MEDLINE; 91067478.
RA MAEGERT H.J., APPELHANS H., GASSEN H.G., FORSSMANN W.G.;
RT "Nucleotide sequence of a porcine prepro atrial natriuretic peptide
RT (ANP) cDNA";
RL NUCLEIC ACIDS RES. 18:6704-6704(1990).
RN [2]
RP SEQUENCE OF 25-150.
RC TISSUE=HEART RIGHT ATRIUM;
RX FORSSMANN W.G., BIRR C., CARLOQUIST M., CHRISTMANN M., FINKE R.,
RA HENSCHEN A., HOCK D., KIRCHHEIM H., KREYE V., LOTTSCHEICH F., METZ J.,
RA MUTT V., REINECKE M.;

RT "the auricular myocardiocytes of the heart constitute an endocrine
RT organ. Characterization of a porcine cardiac peptide hormone,
RT cardiodilatin-126";
RL CELL TISSUE RES. 238:425-430(1984).
CC -!- FUNCTION: ATRIAL NATRIURETIC FACTOR (ANF) IS A POTENT VASOACTIVE
CC SUBSTANCE SYNTHESIZED IN MAMMALIAN ATRIA AND IS THOUGHT TO PLAY A
CC KEY ROLE IN CARDIOVASCULAR HOMEOSTASIS. HAS A CGMP-STIMULATING
CC ACTIVITY.
CC -!- A DISULFIDE BOND IS REQUIRED FOR FULL ACTIVITY OF ATRIOPEPTINS.
CC -!- SIMILARITY: BELONGS TO THE NATRIURETIC PEPTIDES FAMILY.
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CC
CC EMBL; X54669; G1884;
CC PIR; S13107; S13107.
CC PROSITE; PS00263; NATRIURETIC_PEPTIDE; 1.
CC PFAM; PF00212; ANP; 1.
CC VASOACTIVE; SIGNAL. 24
CC SIGNAL 1
CC PEPTIDE 123 150 CARDIODILATIN-RELATED PEPTIDE (CDP)
CC DISULFID 129 145 (BY SIMILARITY).
CC SEQUENCE 150 AA; 16351 MW; 4FF67B94 CRC32;

Query Match 100.0%; Score 41; DB 1; Length 150;
Best Local Similarity 100.0%; Pred. No. 1.76e+01;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DB 146 NSFRY 150
QY 1 NSFRY 5

RESULT 7
ID ANE_MOUSE STANDARD; PRT; 152 AA.
AC P05125;
DT 13-AUG-1987 (REL. 05, CREATED)
DT 13-AUG-1987 (REL. 05, LAST SEQUENCE UPDATE)
DT 01-OCT-1996 (REL. 34, LAST ANNOTATION UPDATE)
DE ATRIAL NATRIURETIC FACTOR PRECURSOR (ANF) (ATRIAL NATRIURETIC PEPTIDE)
DE (ANP) (PREPRONATRIODILATIN).
GN NPPA OR FND.
OS MUS MUSCULUS (MOUSE).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA;
CC RODENTIA; SCIUROGNATHI; MURIDAE; MURINAE; MUS.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE; 85065766.
RA SEIDMAN C.E., BLOCH K.D., KLEIN K.A., SMITH J.A., SEIDMAN J.G.;
RT "Nucleotide sequences of the human and mouse atrial natriuretic
RT factor genes";
RL SCIENCE 226:1206-1209(1984).
CC -!- FUNCTION: ATRIAL NATRIURETIC FACTOR (ANF) IS A POTENT VASOACTIVE
CC SUBSTANCE SYNTHESIZED IN MAMMALIAN ATRIA AND IS THOUGHT TO PLAY A
CC KEY ROLE IN CARDIOVASCULAR HOMEOSTASIS. HAS A CGMP-STIMULATING
CC ACTIVITY.
CC -!- A DISULFIDE BOND IS REQUIRED FOR FULL ACTIVITY OF ATRIOPEPTINS.
CC -!- SIMILARITY: BELONGS TO THE NATRIURETIC PEPTIDES FAMILY.
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CC


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CC EMBL: K02781; G387099; -
DR PIR: A29370; AWMS.
DR MGD: MGI:97367; NPPA.
DR PROSITE: PS00263; NATRIURETIC_PEPTIDE; 1.
DR PFAM: PF00212; ANP; 1.
KW VASOACTIVE; SIGNAL. 24
FT SIGNAL 1 24
FT PEPTIDE 126 149 AURICULIN A (BY SIMILARITY).
FT PEPTIDE 126 150 AURICULIN B (BY SIMILARITY).
FT PEPTIDE 127 149 ATRIOPEPTIN I (BY SIMILARITY).
FT PEPTIDE 127 147 ATRIOPEPTIN II (BY SIMILARITY).
FT DISULFID 129 145 BY SIMILARITY..
SQ SEQUENCE 152 AA; 16645 MW; 5163CB23 CRC32;

Query Match 100.0%; Score 41; DB 1; Length 152;
Best Local Similarity 100.0%; Pred. No. 1.76e+01;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 146 NSFRY 150
QY 1 NSFRY 5
|||||

RESULT 8
ID ANP_BOVIN STANDARD; PRT; 152 AA.
AC P07501;
DT 01-APR-1988 (REL. 07, CREATED)
DT 01-MAR-1989 (REL. 10, LAST SEQUENCE UPDATE)
DT 01-OCT-1996 (REL. 34, LAST ANNOTATION UPDATE)
DE ATRIAL NATRIURETIC FACTOR PRECURSOR (ANP) (ATRIAL NATRIURETIC PEPTIDE)
DE (ANP) (PREPRONATRIODILATIN).
GN NPPA.
OS BOS TAURUS (BOVINE).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA;
OC ARTIODACTYLA; RUMINANTIA; PECORA; BOVIDAE; BOVINAE; BOS.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE; 86215205.
RA VLASUK G.P., MILLER J., BENCEN G.H., LEWICKI J.A.;
RT "Structure and analysis of the bovine atrial natriuretic peptide
precursor gene.";
RL BIOCHEM. BIOPHYS. RES. COMMUN. 136:396-403(1986).
[2]
RP SEQUENCE OF 123-150.
RX MEDLINE; 86173941.
RA ONG H., MCNICOLL N., LAZURE C., SEIDAH N., CHRETIEN M., CANTIN M.,
DE LEAN A.;
RT "Purification and sequence determination of bovine atrial natriuretic
factor.";
RL LIFE SCI. 38:1309-1315(1986).
CC -!- FUNCTION: ATRIAL NATRIURETIC FACTOR (ANP) IS A POTENT VASOACTIVE
SUBSTANCE SYNTHESIZED IN MAMMALIAN ATRIA AND IS THOUGHT TO PLAY A
KEY ROLE IN CARDIOVASCULAR HOMEOSTASIS. HAS A CGMP-STIMULATING
ACTIVITY.
CC -!- A DISULFIDE BOND IS REQUIRED FOR FULL ACTIVITY OF ATRIOPEPTINS.
CC -!- SIMILARITY: BELONGS TO THE NATRIURETIC PEPTIDES FAMILY.
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-----
CC EMBL: M13145; G162666; -
DR PIR: A24247; ANBO.
DR PROSITE: PS00263; NATRIURETIC_PEPTIDE; 1.
DR PFAM: PF00212; ANP; 1.
KW VASOACTIVE; SIGNAL.
FT SIGNAL 1 24
FT PEPTIDE 123 150 ATRIAL NATRIURETIC PEPTIDE, ALPHA (ANP).
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FT DISULFID 129 145
SQ SEQUENCE 152 AA; 16518 MW; CF200882 CRC32;

Query Match 100.0%; Score 41; DB 1; Length 152;
Best Local Similarity 100.0%; Pred. No. 1.76e+01;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 146 NSFRY 150
QY 1 NSFRY 5
|||||

RESULT 9
ID ANP_RAT STANDARD; PRT; 152 AA.
AC P01161;
DT 21-JUL-1986 (REL. 01, CREATED)
DT 21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)
DT 15-DEC-1998 (REL. 37, LAST ANNOTATION UPDATE)
DE ATRIAL NATRIURETIC FACTOR PRECURSOR (ANP) (ATRIAL NATRIURETIC PEPTIDE)
DE (ANP) (PREPRONATRIODILATIN) [CONTAINS: AURICULINS; ATRIOPEPTINS].
GN NPPA.
OS RATTUS NORVEGICUS (RAT).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA;
OC RODENTIA; SCIUROGNATHI; MURIDAE; MURINAE; RATTUS.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE; 84219797.
RA YAMANAKA M., GREENBERG B., JOHNSON L., SEILHAMER J.J., BREWER M.,
RIEDEMANN T., MILLER J., ATLAS S.A., LARAGH J., LEWICKI J.,
FIDDES J.C.;
RT "Cloning and sequence analysis of the cDNA for the rat atrial
natriuretic factor precursor.";
RL NATURE 309:719-722(1984).
[2]
RP SEQUENCE FROM N.A.
RX MEDLINE; 84219798.
RA MAKI M., TAKAYANAGI F., MISONO K.S., PANDEY K.N., TIBBETTS C.,
INAGAMI T.;
RT "Structure of rat atrial natriuretic factor precursor deduced from
cDNA sequence.";
RL NATURE 309:722-724(1984).
[3]
RP SEQUENCE FROM N.A.
RX MEDLINE; 84250178.
RA SEIDMAN C.E., DUBY A.D., CHOI E., GRAHAM R.M., HABER E., HOMCY C.,
SMITH J.A., SEIDMAN J.G.;
RT "The structure of rat preproatrial natriuretic factor as defined by a
complementary DNA clone.";
RL SCIENCE 225:324-326(1984).
[4]
RP SEQUENCE FROM N.A.
RX MEDLINE; 85061500.
RA KANGAWA K., TAWARAGI Y., OIKAWA S., MIZUNO A., SAKURAGAWA Y.,
KANAZATO H., FUKUDA A., MINAMINO N., MATSUO H.;
RT "Identification of rat gamma atrial natriuretic polypeptide and
characterization of the cDNA encoding its precursor.";
RL NATURE 312:152-155(1984).
[5]
RP SEQUENCE FROM N.A.
RX MEDLINE; 85182558.
RA ARGENTIN S., NEMER M., DROUIN J., SCOTT G.K., KENNEDY B.P.,
DAVIES P.L.;
RT "The gene for rat atrial natriuretic factor.";
RL J. BIOL. CHEM. 260:4568-4571(1985).
[6]
RP SEQUENCE FROM N.A.
RX MEDLINE; 85038509.
RA ZIVIN R.A., CONDERA J.H., DIXON R.A.F., SEIDAH N.G., CHRETIEN M.,
NEMER M., CHAMBERLAND M., DROUIN J.;
RT "Molecular cloning and characterization of DNA sequences encoding rat
and human atrial natriuretic factors.";
RL PROC. NATL. ACAD. SCI. U.S.A. 81:6325-6329(1984).
[7]
```

RP SEQUENCE FROM N.A.
RX MEDLINE; 86109092.
RA FLYNN T.G.;
RT "The elucidation of the structure of atrial natriuretic factor, a new peptide hormone."
RL CAN. J. PHYSIOL. PHARMACOL. 65:2013-2020(1987).
RN [8]
RP SEQUENCE OF 38-152 FROM N.A.
RX MEDLINE; 87175636.
RA GARDNER D.G., VLASUK G.P., BAXTER J.D., FIDDES J.C., LEWICKI J.A.;
RT "Identification of atrial natriuretic factor gene transcripts in the central nervous system of the rat."
RL PROC. NATL. ACAD. SCI. U.S.A. 84:2175-2179(1987).
RN [9]
RP AURICULINS, SEQUENCE, AND SYNTHESIS OF 126-149.
RX MEDLINE; 84219796.
RA ATLAS S.A., KLEINERT H.D., CAMARGO M.J., JANUSZEWICZ A., SEALEY J.E., LARACH J.H., SCHILLING J.W., LEWICKI J.A., JOHNSON L.K., MAACK T.;
RT "Purification, sequencing and synthesis of natriuretic and vasoactive rat atrial peptide."
RL NATURE 309:717-719(1984).
RN [10]
RP SEQUENCE OF 127-149, AND SYNTHESIS.
RX MEDLINE; 84097513.
RA CURRIE M.G., GELLER D.M., COLE B.R., SIEGEL N.R., FOX K.F., ADAMS S.P., EUBANKS S.R., GALLOPPI G.R., NEEDLEMAN P.;
RT "Purification and sequence analysis of bioactive atrial peptides (atriopeptins)."
RL SCIENCE 223:67-69(1984).
RN [11]
RP SEQUENCE OF 118-150.
RX MEDLINE; 84194062.
RA SEIDAH N.G., LAZURE C., CHRETIEN M., THIBAUT G., GARCIA R., CANTIN M., GENEST J., NUTT R.F., BRADY S.F., LYLE T.A., PALEVEDA W.J., COLTON C.D., CICCARONE T.M., VEBER D.F.;
RT "Amino acid sequence of homologous rat atrial peptides: natriuretic activity of native and synthetic forms."
RL PROC. NATL. ACAD. SCI. U.S.A. 81:2640-2644(1984).
RN [12]
RP SEQUENCE OF 25-38.
RX MEDLINE; 88203350.
RA THIBAUT G., MURPHY K.K., GUTKOWSKA J., SEIDAH N.G., LAZURE C., CHRETIEN M., CANTIN M.;
RT "NH2-terminal fragment of rat pro-atrial natriuretic factor in the circulation: identification, radioimmunoassay and half-life."
RL PEPTIDES 9:47-53(1988).
CC -1- FUNCTION: ATRIAL NATRIURETIC FACTOR (ANF) IS A POTENT VASOACTIVE SUBSTANCE SYNTHESIZED IN MAMMALIAN ATRIA AND IS THOUGHT TO PLAY A KEY ROLE IN CARDIOVASCULAR HOMEOSTASIS. HAS A CGMP-STIMULATING ACTIVITY.
CC -1- A DISULFIDE BOND IS REQUIRED FOR FULL ACTIVITY OF ATRIOPEPTINS.
CC -1- SIMILARITY: BELONGS TO THE NATRIURETIC PEPTIDES FAMILY.
CC
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CC
CC EMBL; M15868; G202904;
CC EMBL; X00665; G55712;
CC EMBL; X02062; G202900;
CC EMBL; X01118; G55717;
CC EMBL; M27498; G202906;
CC PIR; A22570; AWRT.
CC PIR; A44190; A44190.
CC PROSITE; PS00263; NATRIURETIC_PEPTIDE; 1.
CC PFAM; PF00212; ANP; 1.
CC VASOACTIVE; SIGNAL. 24
CC SIGNAL 126 149 AURICULIN A.
CC PEPTIDE

FT PEPTIDE 126 150 AURICULIN B.
FT PEPTIDE 127 147 ATRIOPEPTIN I.
FT PEPTIDE 127 149 ATRIOPEPTIN II.
FT PEPTIDE 127 150 ATRIOPEPTIN III.
FT DISULFID 129 145
SQ SEQUENCE 152 AA; 16556 MW; 2D424B75 CRC32;
Query Match 100.0%; Score 41; DB 1; Length 152;
Best Local Similarity 100.0%; Pred. No. 1.76e+01;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Db 146 NSFRY 150
QY 1 NSFRY 5
RESULT 10
ID ANF_RABBIT STANDARD; PRT; 153 AA.
AC P07500;
DT 01-APR-1988 (REL. 07, CREATED)
DT 01-APR-1988 (REL. 07, LAST SEQUENCE UPDATE)
DE 01-OCT-1996 (REL. 34, LAST ANNOTATION UPDATE)
DE ATRIAL NATRIURETIC FACTOR PRECURSOR (ANF) (ATRIAL NATRIURETIC PEPTIDE)
DE (ANP) (PREPRONATRIODILATIN).
GN NPPA.
OS ORYCTOLAGUS CUNICULUS (RABBIT).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA;
OC LAGOMORPHA; LEPORIDAE; ORYCTOLAGUS.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE; 86076957.
RA OIKAWA S., IMAI M., INUZUKA C., TAWARAGI Y., NAKAZATO H., MATSUO H.;
RT "Structure of dog and rabbit precursors of atrial natriuretic polypeptides deduced from nucleotide sequence of cloned cDNA."
RL BIOCHEM. BIOPHYS. RES. COMMUN. 132:892-899(1985).
CC -1- FUNCTION: ATRIAL NATRIURETIC FACTOR (ANF) IS A POTENT VASOACTIVE SUBSTANCE SYNTHESIZED IN MAMMALIAN ATRIA AND IS THOUGHT TO PLAY A KEY ROLE IN CARDIOVASCULAR HOMEOSTASIS. HAS A CGMP-STIMULATING ACTIVITY.
CC -1- A DISULFIDE BOND IS REQUIRED FOR FULL ACTIVITY OF ATRIOPEPTINS.
CC -1- SIMILARITY: BELONGS TO THE NATRIURETIC PEPTIDES FAMILY.
CC
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CC
CC EMBL; M12045; G164771;
CC PIR; B25302; AWRB.
CC PROSITE; PS00263; NATRIURETIC_PEPTIDE; 1.
CC PFAM; PF00212; ANP; 1.
CC VASOACTIVE; SIGNAL. 25
CC SIGNAL 124 151 ATRIAL NATRIURETIC PEPTIDE, ALPHA (ANP).
FT PEPTIDE 124 151
FT DISULFID 130 146
SQ SEQUENCE 153 AA; 16843 MW; 1FA4FB42 CRC32;
Query Match 100.0%; Score 41; DB 1; Length 153;
Best Local Similarity 100.0%; Pred. No. 1.76e+01;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Db 147 NSFRY 151
QY 1 NSFRY 5
RESULT 11
ID ANF_HUMAN STANDARD; PRT; 153 AA.
AC P01160;
DT 21-JUL-1986 (REL. 01, CREATED)

DT 13-AUG-1987 (REL. 05, LAST SEQUENCE UPDATE)
DT 15-DEC-1998 (REL. 37, LAST ANNOTATION UPDATE)
DE ATRIAL NATRIURETIC FACTOR PRECURSOR (ANF) (ATRIAL NATRIURETIC PEPTIDE)
DE (ANP) (PREPRONATRIODILATIN).
GN NPPA OR PND.
OS HOMO SAPIENS (HUMAN).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA;
OC PRIMATES; CATARRHINI; HOMINIDAE; HOMO.
RN [1]
RP SEQUENCE OF 1-151 FROM N.A.
RX MEDLINE; 84219799.
RA OIKAWA S., INAI M., UENO A., TANAKA S., NOGUCHI T., NAKAZATO H.,
RA KANGAWA K., FUKUDA A., MATSUO H.: cDNA encoding a precursor for human
RT atrial natriuretic polypeptide.";
RL NATURE 309:724-726(1984).
RN [2]
RP SEQUENCE OF 1-151 FROM N.A.
RX MEDLINE; 84295577.
RA NAKAYAMA K., OHKUBO H., HIROSE T., INAYAMA S., NAKANISHI S.:
RT "mRNA sequence for human cardiodilatin-atrial natriuretic factor
RT precursor and regulation of precursor mRNA in rat atria.";
RL NATURE 310:699-701(1984).
RN [3]
RP SEQUENCE OF 1-151 FROM N.A.
RX MEDLINE; 85061626.
RA NEMER M., CHAMBERLAND M., SIROIS D., ARGENTIN S., DROUIN J.,
RA DIXON R.A.F., ZIVIN R.A., CONDRA J.H.:
RT "Gene structure of human cardiac hormone precursor,
RT pronatriodilatin.";
RL NATURE 312:654-656(1984).
RN [4]
RP SEQUENCE OF 1-151 FROM N.A.
RX MEDLINE; 85061627.
RA GREENBERG B.D., BENGEN G.H., SEILHAMER J.J., LEWICKI J.A.,
RA FIDES J.C.:
RT "Nucleotide sequence of the gene encoding human atrial natriuretic
RT factor precursor.";
RL NATURE 312:656-658(1984).
RN [5]
RP SEQUENCE OF 1-151 FROM N.A.
RX MEDLINE; 85065766.
RA SEIDMAN C.E., BLOCH K.D., KLEIN K.A., SMITH J.A., SEIDMAN J.G.:
RT "Nucleotide sequences of the human and mouse atrial natriuretic
RT factor genes.";
RL SCIENCE 226:1206-1209(1984).
RN [6]
RP SEQUENCE OF 1-151 FROM N.A.
RX ERRINGTON H.:
RL SUBMITTED (MAY-1998) TO EMBL/GENBANK/DBJ DATA BANKS.
RN [7]
RP SEQUENCE OF 118-153 FROM N.A.
RX MEDLINE; 85038509.
RA ZIVIN R.A., CONDRA J.H., DIXON R.A.F., SEIDAH N.G., CHRETIEN M.,
RA NEMER M., CHAMBERLAND M., DROUIN J.:
RT "Molecular cloning and characterization of DNA sequences encoding rat
RT and human atrial natriuretic factors.";
RL PROC. NATL. ACAD. SCI. U.S.A. 81:6325-6329(1984).
RN [8]
RP SEQUENCE OF 1-75 FROM N.A.
RX MEDLINE; 85096983.
RA MAKI M., PARMENTIER M., INAGAMI T.:
RT "Cloning of genomic DNA for human atrial natriuretic factor.";
RL BIOCHEM. BIOPHYS. RES. COMMUN. 125:797-802(1984).
RN [9]
RP SEQUENCE OF 124-151.
RX MEDLINE; 84128019.
RA KANGAWA K., MATSUO H.:
RT "Purification and complete amino acid sequence of alpha-human atrial
RT natriuretic polypeptide (alpha-hANP).";
RL BIOCHEM. BIOPHYS. RES. COMMUN. 118:131-139(1984).
RN [10]
RP STRUCTURE BY NMR OF 124-151 MUTANT SELECTIVE FOR NPR-C RECEPTOR.

RX MEDLINE; 94318633.
RA FAIRBROTHER W.J., MCDOWELL R.S., CUNNINGHAM B.C.:
RT "Solution conformation of an atrial natriuretic peptide variant
RT selective for the type A receptor.";
RL BIOCHEMISTRY 33:8897-8904(1994).
CC -!- FUNCTION: ATRIAL NATRIURETIC FACTOR (ANF) IS A POTENT VASOACTIVE
CC SUBSTANCE SYNTHESIZED IN MAMMALIAN ATRIA AND IS THOUGHT TO PLAY A
CC KEY ROLE IN CARDIOVASCULAR HOMEOSTASIS. HAS A COMP-STIMULATING
CC ACTIVITY.
CC -!- THE HUMAN GENOME CONTAINS 2 DIFFERENT PREPRONATRIODILATIN GENES
CC ONE CODES FOR 2 ARG RESIDUES AT THE C-TERMINUS THAT ARE CLEAVED
CC TO FORM THE MATURE PEPTIDE, WHILE THE OTHER ENDS IN A TERMINATION
CC CODON IMMEDIATELY AFTER THE LAST CODON OF THE MATURE PEPTIDE.
CC -!- SIMILARITY: BELONGS TO THE NATRIURETIC PEPTIDES FAMILY.
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CC -----
DR EMBL; X01470; G825625; -
DR EMBL; X02558; G825625; JOINED.
DR EMBL; K02043; G178630; -
DR EMBL; X01471; E27452; ALT_SEQ.
DR EMBL; K02044; G178632; -
DR EMBL; AL021155; E1294859; -
DR EMBL; M30262; G180182; -
DR EMBL; K02399; G178634; -
DR PIR; A01424; ANHU
DR PIR; A22693; A22693.
DR PIR; A32733; A32733.
DR PDB; 1ANP; 07-APR-95.
DR MIM; 108780; -
DR PROSITE; PS00263; NATRIURETIC_PEPTIDE; 1.
DR PFAM; PF00212; ANP; 1
KW VASOACTIVE; SIGNAL; 3D-STRUCTURE.
FT SIGNAL 1 25
FT PEPTIDE 26 55 CARDIODILATIN-RELATED PEPTIDE (CDP).
FT PEPTIDE 124 151 ATRIAL NATRIURETIC PEPTIDE, ALPHA (ANP).
FT DISULFID 130 146 BY SIMILARITY.
FT VARIANT 152 153 MISSING (IN ONE OF THE TWO GENES).
SQ SEQUENCE 153 AA; 16708 MW; C24A68AF CRC32.

Query Match 100.0%; Score 41; DB 1; Length 153;
Best Local Similarity 100.0%; Pred. No. 1.76e+01;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 147 NSFRY 151
Qy 1 NSFRY 5
|||||

RESULT 12
ID ANF_HORSE STANDARD; PRT; 153 AA.
AC P27104;
DT 01-AUG-1992 (REL. 23, CREATED)
DT 01-AUG-1992 (REL. 23, LAST SEQUENCE UPDATE)
DT 01-OCT-1996 (REL. 34, LAST ANNOTATION UPDATE)
DE ATRIAL NATRIURETIC FACTOR PRECURSOR (ANF) (ATRIAL NATRIURETIC PEPTIDE)
DE (ANP) (PREPRONATRIODILATIN).
GN NPPA.
OS EQUUS CABALLUS (HORSE).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA;
OC PERISSODACTYLA; EQUIDAE; EQUUS.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-ADAMITICUS; TISSUE-HEART ATRIUM;
RA MAERGERT H.J., RICHTER R., SCHMAEDING G., FORSSMANN W.G.:
RL SUBMITTED (MAR-1991) TO EMBL/GENBANK/DBJ DATA BANKS.
CC -!- FUNCTION: ATRIAL NATRIURETIC FACTOR (ANF) IS A POTENT VASOACTIVE

CC SUBSTANCE SYNTHESIZED IN MAMMALIAN ATRIA AND IS THOUGHT TO PLAY A
CC KEY ROLE IN CARDIOVASCULAR HOMEOSTASIS. HAS A CGMP-STIMULATING
CC ACTIVITY.
CC -|- A DISULFIDE BOND IS REQUIRED FOR FULL ACTIVITY OF ATRIOPEPTINS.
CC -|- SIMILARITY: BELONGS TO THE NATRIURETIC PEPTIDES FAMILY.
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CC -----
DR EMBL; X58563; G1009; -
DR PIR; S14873; S14873.
DR PROSITE; PS00263; NATRIURETIC_PEPTIDE; 1.
DR PFAM; PF00212; ANP; 1.
KW VASOACTIVE; SIGNAL. 25
FT SIGNAL 1
FT PEPTIDE 124 151 ATRIAL NATRIURETIC PEPTIDE, ALPHA (ANP).
FT DISULFID 130 146 BY SIMILARITY.
SQ SEQUENCE 153 AA; 16825 MW; FESD5F4A CRC32;

Query Match 100.0%; Score 41; DB 1; Length 153;
Best Local Similarity 100.0%; Pred. No. 1.76e+01;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 147 NSFRY 151
|||||
QY 1 NSFRY 5

RESULT 13
ID PFLCLOPA STANDARD; PRT; 740 AA.
AC Q46266;
DT 01-NOV-1997 (REL. 35, CREATED)
DT 01-NOV-1997 (REL. 35, LAST SEQUENCE UPDATE)
DT 01-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE)
DE FORMATE ACETYLTRANSFERASE (EC 2.3.1.54) (PYRUVATE FORMATE-LYASE).
GN PFL.
OS CLOSTRIDIUM PASTEURIANUM.
OC BACTERIA; FIRMICUTES; BACILLUS/CLOSTRIDIUM GROUP; CLOSTRIDIACEAE;
OC CLOSTRIDIUM.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE; 96218720.
RA WEIDNER G., SAWERS G.;
RT Molecular characterization of the genes encoding pyruvate
RT formate-lyase and its activating enzyme of Clostridium
RT pasteurianum.";
RL J. BACTERIOL. 178:2440-2444(1996).
CC -|- CATALYTIC ACTIVITY: ACETYL-COA + FORMATE - COA + PYRUVATE.
CC -|- PATHWAY: GLUCOSE METABOLISM (NONOXIDATIVE CONVERSION).
CC -|- SUBUNIT: HOMODIMER (BY SIMILARITY).
CC -|- SUBCELLULAR LOCATION: CYTOPLASMIC (BY SIMILARITY).
CC -|- SIMILARITY: STRONG, TO OTHER PYRUVATE FORMATE-LYASES.
CC -----
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CC -----
DR EMBL; X93463; G1072361; -
DR PROSITE; PS00850; GLY_RADICAL; 1.
DR PFAM; PF01228; GLY_radical; 1.
KW TRANSFERASE; ACYLTRANSFERASE; GLUCOSE METABOLISM; ORGANIC RADICAL.
FT MOD_RES 715 715 FREE RADICAL (BY SIMILARITY).
SQ SEQUENCE 740 AA; 83216 MW; 4CE5E8C5 CRC32;

Query Match 100.0%; Score 41; DB 1; Length 740;
Best Local Similarity 100.0%; Pred. No. 1.76e+01;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 340 NSFRY 344
|||||
QY 1 NSFRY 5

RESULT 14
ID TDCE ECOLI STANDARD; PRT; 746 AA.
AC P42632;
DT 01-NOV-1995 (REL. 32, CREATED)
DT 01-NOV-1995 (REL. 32, LAST SEQUENCE UPDATE)
DT 15-JUL-1998 (REL. 36, LAST ANNOTATION UPDATE)
DE KETO-ACID FORMATE ACETYLTRANSFERASE (EC 2.3.1.-) (KETO-ACID FORMATE-
DE LYASE).
GN TDCE.
OS ESCHERICHIA COLI.
OC BACTERIA; PROTEOBACTERIA; GAMMA SUBDIVISION; ENTEROBACTERIACEAE;
OC ESCHERICHIA.
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN-K12 / MG1655;
RX MEDLINE; 97426617.
RA BLATTNER F.R., PLUNKETT G. III, BLOCH C.A., PERNA N.T., BURLAND V.,
RA RILEY M., COLLADO-VIDES J., GLASNER F.D., RODE C.K., MAYHEW G.F.,
RA GREGOR J., DAVIS N.W., KIRKPATRICK H.A., GOEDEN M.A., ROSE D.J.,
RA MAU B., SHAO Y.;
RT "The complete genome sequence of Escherichia coli K-12".
RL Science 277:1453-1474(1997).
RN [2]
RP CHARACTERIZATION.
RA HESSLINGER C., FAIRHURST S.A., SAWERS G.;
RL UNPUBLISHED OBSERVATIONS (XXX-1997).
CC -|- PATHWAY: ANAEROBIC PATHWAY THAT DEGRADES L-THREONINE TO
CC PROPIONATE.
CC -|- SUBCELLULAR LOCATION: CYTOPLASMIC (BY SIMILARITY).
CC -|- SIMILARITY: STRONG, TO PYRUVATE FORMATE-LYASES.
CC -----
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CC -----
DR EMBL; U18997; G606055; -
DR EMBL; AE000393; G1789502; -
DR ECOGENE; EG12758; TDCE.
DR PROSITE; PS00850; GLY_RADICAL; 1.
DR PFAM; PF01228; GLY_radical; 1.
KW TRANSFERASE; ACYLTRANSFERASE; ORGANIC RADICAL.
FT MOD_RES 739 739 FREE RADICAL (BY SIMILARITY).
SQ SEQUENCE 746 AA; 83731 MW; DA3FA991 CRC32;

Query Match 100.0%; Score 41; DB 1; Length 746;
Best Local Similarity 100.0%; Pred. No. 1.76e+01;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 357 NSFRY 361
|||||
QY 1 NSFRY 5

RESULT 15
ID YAC1 MAIZE STANDARD; PRT; 102 AA.
AC P08771;
DT 01-NOV-1988 (REL. 09, CREATED)
DT 01-NOV-1988 (REL. 09, LAST SEQUENCE UPDATE)
DT 15-DEC-1998 (REL. 37, LAST ANNOTATION UPDATE)
DE TRANSPOSABLE ELEMENT ACTIVATOR HYPOTHETICAL 12 KD PROTEIN (AC 12 KD

```

DE PROTEIN).
OS ZEA MAYS (MAIZE).
OC EUKARYOTA; VIRIDIPHYTES; STREPTOPHYTA; EMBRYOPHYTA; TRACHEOPHYTA;
OC EUPHYLLOPHYTES; SPERMATOPHYTA; MAGNOLIOPHYTA; LILIOPSIDA; POALES;
OC POACEAE; ZEA.
RN [1]
RP SEQUENCE FROM N.A.
RA KUNZE R., STOCHAJ U., LAUFS J., STARLINGER P.;
RT "Transcription of transposable element Activator (Ac) of Zea mays L.";
RL EMBO J. 6:1555-1563(1987).
CC -!- THIS PROTEIN IS CODED BY THE TRANSPOSABLE MAIZE CONTROLLING
CC ELEMENT "ACTIVATOR" (AC), WHICH IS ABLE TO ACTIVATE CHROMOSOME
CC BREAKAGE AT A SPECIFIC LOCATION.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; X05424; G22114; -
CC PIR; A27863; A27863.
CC MAIZEDB; 69192; -
CC TRANSPOSABLE ELEMENT; HYPOTHETICAL PROTEIN.
SQ SEQUENCE 102 AA; 12406 MW; 1AE0E76C CRC32;

Query Match 95.1%; Score 39; DB 1; Length 102;
Best Local Similarity 80.0%; Pred. No. 5.00e+01;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Db 71 NTRY 75
QY 1 NSRY 5

Search completed: Wed Jun 16 13:23:53 1999
Job time : 7 secs.

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WATERMAN (TM)

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MPsrch_pp protein - protein database search, using Smith-Waterman algorithm
Run on: Wed Jun 16 13:24:09 1999; MasPar time 4.08 Seconds
66.914 Million cell updates/sec
Tabular output not generated.

Title: >US-09-027-777B-3
Description: (1-5) from US09027777B.pep
Perfect Score: 41
Sequence: 1 NSFRY 5

Scoring table: PAM 150
Gap 15

Searched: 179066 seqs, 54579741 residues

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database: sprembl9
1:sp_archaea 2:sp_bacteria 3:sp_fungi 4:sp_human
5:sp_invertebrate 6:sp_mammal 7:sp_mhc 8:sp_Organelle
9:sp_phase 10:sp_plant 11:sp_rodent 12:sp_unclassified
13:sp_vertebrate 14:sp_virus

Statistics: Mean 20.285; Variance 23.245; scale 0.873

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description	Pred. No.
1	41	100.0	110	1	058195	110AA LONG HYPOTHETICA 5.47e+01
2	41	100.0	151	4	Q13766	ATRIAL NATRIURETIC FAC 5.47e+01
3	41	100.0	152	6	O46540	ATRIAL NATRIURETIC PEP 5.47e+01
4	41	100.0	155	6	Q29130	CARDIODILATIN, ATRIAL 5.47e+01
5	41	100.0	164	8	P92530	ORF164. 5.47e+01
6	41	100.0	195	5	O44830	F54D12.6 PROTEIN 5.47e+01
7	41	100.0	513	2	O32561	KETO ACID FORMATE-LYAS 5.47e+01
8	41	100.0	635	10	O84715	T8K22.8 PROTEIN. 5.47e+01
9	41	100.0	993	5	P91157	COSMID C44C3.. 5.47e+01
10	39	95.1	79	2	O56386	HYPOTHETICAL 9.2 KD PR 1.41e+02
11	39	95.1	107	1	O58090	107AA LONG HYPOTHETICA 1.41e+02
12	39	95.1	141	10	P93305	ORF141. 1.41e+02
13	39	95.1	190	5	O77421	FEMALE-SPECIFIC HISTAM 1.41e+02
14	39	95.1	209	14	O12300	REPLICASE. 1.41e+02
15	39	95.1	240	2	O31875	YOSIN PROTEIN. 1.41e+02
16	39	95.1	254	13	Q91307	MYOSIN VI (FRAGMENT). 1.41e+02
17	39	95.1	256	5	O61766	C35E7.8 PROTEIN. 1.41e+02
18	39	95.1	293	14	O96615	BV1 AND BCL GENES, COM 1.41e+02
19	39	95.1	297	13	Q91296	MYOSIN VI (FRAGMENT). 1.41e+02
20	39	95.1	310	2	O66675	ADP-L-GLYCERO-D-MANNO- 1.41e+02

21	39	95.1	315	5	O61946	T24A6.4 PROTEIN. 1.41e+02
22	39	95.1	331	5	O46031	CYSTEINE PROTEINASE. 1.41e+02
23	39	95.1	331	5	O46032	CYSTEINE PROTEINASE. 1.41e+02
24	39	95.1	338	5	O46030	CYSTEINE PROTEINASE. 1.41e+02
25	39	95.1	341	5	O95029	CYSTEINE PROTEINASE 1 1.41e+02
26	39	95.1	350	5	O76720	F36H12.2 PROTEIN. 1.41e+02
27	39	95.1	360	1	P96085	GTP-BINDING PROTEIN. 1.41e+02
28	39	95.1	375	2	O30877	M.BSSHII METHYLASE. 1.41e+02
29	39	95.1	439	2	O05912	HYPOTHETICAL 48.7 KD P 1.41e+02
30	39	95.1	453	2	O13383	NOSD PROTEIN. 1.41e+02
31	39	95.1	517	3	O13606	HNF-3/FORK-HEAD TRANSC 1.41e+02
32	39	95.1	569	1	O62270	F58G1.7 PROTEIN. 1.41e+02
33	39	95.1	589	1	O58168	589AA LONG HYPOTHETICA 1.41e+02
34	39	95.1	614	5	O46149	WEEL-LIKE KINASE. 1.41e+02
35	39	95.1	671	5	O21046	F59F5.3 PROTEIN. 1.41e+02
36	39	95.1	724	2	P94274	UNIDENTIFIED FERRIC SI 1.41e+02
37	39	95.1	729	14	O12301	REPLICASE. 1.41e+02
38	39	95.1	793	3	O14073	PUTATIVE DIPEPTIDYL AM 1.41e+02
39	39	95.1	803	2	O45755	DELTA-ENDOTOXIN. 1.41e+02
40	39	95.1	863	2	P72599	FERRICROMONE-IRON RECP 1.41e+02
41	39	95.1	1064	2	O50302	CARBOMYLPHOSPHATE SYNT 1.41e+02
42	39	95.1	1072	3	O13807	HYPOTHETICAL 120.7 KD 1.41e+02
43	39	95.1	1149	11	O54705	INDUCIBLE NITRIC OXIDE 1.41e+02
44	39	95.1	1510	9	O80179	PUTATIVE MINOR TAIL PR 1.41e+02
45	39	95.1	1517	2	O34071	ORF40. 1.41e+02

ALIGNMENTS

RESULT 1
ID O58195 PRELIMINARY; PRT; 110 AA.
AC O58195;
DT 01-AUG-1998 (TREMBLREL. 07, CREATED)
DT 01-AUG-1998 (TREMBLREL. 07, LAST SEQUENCE UPDATE)
DT 01-JAN-1999 (TREMBLREL. 09, LAST ANNOTATION UPDATE)
DE 110AA LONG HYPOTHETICAL PROTEIN.
GN PH0480
OS PYROCOCCLUS HORIKOSHII.
OC ARCHAEA; EURYARCHAEOTA; THERMOCOCCALES; THERMOCOCCACEAE; PYROCOCCLUS.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=OT3.
RX MEDLINE: 98344137.
RA KAWARABAYASHI Y., SAWADA M., HORIKAWA H., HAIKAWA Y., HINO Y.,
RA YAMAMOTO S., SEKINE M., BABA S., KOSUGI H., HOSOKAWA A., NAGAI Y.,
RA SAKAI M., OGURA K., OTUKA R., NAKAZAWA H., TAKAMIYA M., OHFUKU Y.,
RA FUNAHASHI T., TANAKA T., KUDOH Y., YAMAZAKI J., KUSHIDA N., OGUCHI A.,
RA AOKI K., NAKAMURA Y., ROBB T.F., HORIKOSHI K., MASUCHI Y., SHIZUYA H.,
RA KIKUCHI H.;
RT *Complete Sequence and Gene Organization of the Genome of a
RT Hyper-thermophilic Archaeobacterium, Pyrococcus horikoshii OT3.*;
RL DNA RES. 5:55-76(1998).
DR EMBL: AF000002; D1030511;
SQ SEQUENCE 110 AA, 12260 MW; 7F91E1F6 CRC32;
Query Match 100.0%; Score 41; DB 1; Length 110;
Best Local Similarity 100.0%; Pred. No. 5.47e+01;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 54 NSFRY 58
| | | | |
QY 1 NSFRY 5
RESULT 2
ID Q13766 PRELIMINARY; PRT; 151 AA.
AC Q13766;
DT 01-NOV-1996 (TREMBLREL. 01, CREATED)
DT 01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)
DT 01-JAN-1999 (TREMBLREL. 09, LAST ANNOTATION UPDATE)
DE ATRIAL NATRIURETIC FACTOR PRECURSOR.
OS HOMO SAPIENS (HUMAN).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA; PRIMATES;

OC CATARRHINI; HOMINIDAE; HOMO.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE; 85206210.
RA SEIDMAN C.E., BLOCH K.D., ZISFEIN J., SMIT J., HABER E., HOWCY C.,
RA DUBY A.D., CHOI E., GRAHAM R.M., SEIDMAN J.G.;
RT "Molecular studies of the atrial natriuretic factor gene."
RL HYPERTENSION 7:31-34(1985).
DR EMBL; M54947; G178638;
DR EMBL; M54951; G178638; JOINED.
DR PROSITE; PS00263; NATRIURETIC_PEPTIDE; 1.
DR PFAM; PF00212; ANP; 1.
KW VASOACTIVE; SIGNAL.
FT SIGNAL 1 25
FT PEPTIDE 26 55
FT PEPTIDE 124 151
FT DISULFID 130 146
SQ SEQUENCE 151 AA; 16381 MW; E8827DA3 CRC32;
Query Match 100.0%; Score 41; DB 4; Length 151;
Best Local Similarity 100.0%; Pred. No. 5.47e+01;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Db 147 NSFRY 151
Qy 1 NSFRY 5
RESULT 3
ID O46540 PRELIMINARY; PRT: 152 AA.
AC O46540;
DT 01-JUN-1998 (TREMBLREL. 06, CREATED)
DT 01-JUN-1998 (TREMBLREL. 06, LAST SEQUENCE UPDATE)
DT 01-AUG-1998 (TREMBLREL. 07, LAST ANNOTATION UPDATE)
DE ATRIAL NATRIURETIC PEPTIDE.
GN ANP.
OS OVIS ARIES (SHEEP).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA;
OC ARTIODACTYLA; RUMINANTIA; PECORA; BOVOIDEA; BOVIDAE; CAPRINAE; OVIS.
RN [1]
RP SEQUENCE FROM N.A.
RA AITKEN G.D., RAIZIS A.M., GEORGE P.M., ESPINER E.A., CAMERON V.A.;
RL SUBMITTED (DEC-1997) TO EMBL/GENBANK/DBJ DATA BANKS.
DR EMBL; AF037465; G2708650;
DR PROSITE; PS00263; NATRIURETIC_PEPTIDE; 1.
SQ SEQUENCE 152 AA; 16368 MW; D5360BCC CRC32;
Query Match 100.0%; Score 41; DB 6; Length 152;
Best Local Similarity 100.0%; Pred. No. 5.47e+01;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Db 146 NSFRY 150
Qy 1 NSFRY 5
RESULT 4
ID Q29130 PRELIMINARY; PRT: 155 AA.
AC Q29130;
DT 01-NOV-1996 (TREMBLREL. 01, CREATED)
DT 01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)
DT 01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)
DE CARDIOLATIN, ATRIAL NATRIURETIC PEPTIDE.
OS TUPAIA BELANGERI.
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA;
OC SCANDENTIA; TUPAIDAE; TUPAIA.
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE-HEART;
RA SCHNEIDMANN S., MAEGERT H.J., FORSSMANN W.G.;
RL SUBMITTED (MAR-1996) TO EMBL/GENBANK/DBJ DATA BANKS.
RN [2]
RP SEQUENCE FROM N.A.

RC TISSUE-HEART;
RA PARDIGOL A.;
RL SUBMITTED (MAR-1996) TO EMBL/GENBANK/DBJ DATA BANKS.
DR EMBL; Z70294; E233859;
DR PROSITE; PS00263; NATRIURETIC_PEPTIDE; 1.
DR PFAM; PF00212; ANP; 1.
SQ SEQUENCE 155 AA; 16860 MW; 77E8CA8B CRC32;
Query Match 100.0%; Score 41; DB 6; Length 155;
Best Local Similarity 100.0%; Pred. No. 5.47e+01;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Db 149 NSFRY 153
Qy 1 NSFRY 5
RESULT 5
ID P92530 PRELIMINARY; PRT: 164 AA.
AC P92530;
DT 01-MAY-1997 (TREMBLREL. 03, CREATED)
DT 01-MAY-1997 (TREMBLREL. 03, LAST SEQUENCE UPDATE)
DT 01-MAY-1997 (TREMBLREL. 03, LAST ANNOTATION UPDATE)
DE ORF164.
OS ARABIDOPSIS THALIANA (MOUSE-EAR CRESS).
OG MITOCHONDRION.
OC EUKARYOTA; VIRIDIPLANTAE; STREPTOPHYTA; EMBRYOPHYTA; TRACHEOPHYTA;
OC EUPHYLLIPHYTES; SPERMATOPHYTA; MAGNOLIOPHYTA; EUDICOTYLEDONS; ROSIDAE;
OC CAPPARALES; BRASSICACEAE; ARABIDOPSIS.
RN [1]
RP SEQUENCE FROM N.A.
RA UNSELD M., MARIENFELD J.R., BRANDT P., BRENNICKE A.;
RL NAT. GENET. 0:0-0(0).
DR EMBL; Y08502; E283579;
KW MITOCHONDRION.
SQ SEQUENCE 164 AA; 18341 MW; E294F940 CRC32;
Query Match 100.0%; Score 41; DB 8; Length 164;
Best Local Similarity 100.0%; Pred. No. 5.47e+01;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Db 149 NSFRY 153
Qy 1 NSFRY 5
RESULT 6
ID O44830 PRELIMINARY; PRT: 195 AA.
AC O44830;
DT 01-JUN-1998 (TREMBLREL. 06, CREATED)
DT 01-JUN-1998 (TREMBLREL. 06, LAST SEQUENCE UPDATE)
DT 01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)
DE F54D12.6 PROTEIN.
GN F54D12.6.
OS CAENORHABDITIS ELEGANS.
OC EUKARYOTA; METAZOA; NEMATODA; SECERNENTEA; RHABDITIA; RHABDITIDA;
OC RHABDITINA; RHABDITOIDEA; RHABDITIDAE; PELODERINAE; CAENORHABDITIS.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-BRISTOL N2;
RX MEDLINE; 94150718.
RA WILSON R., AINSOUGH R., ANDERSON K., BAYNES C., BERKS M.,
RA BONFIELD J., BURTON J., CONNELL M., COPSEY T., COOPER J., COULSON A.,
RA CRAXTON M., DEAR S., DU Z., DURBIN R., FAVELO A., FULTON L.,
RA GARDNER A., GREEN P., HAWKINS T., HILLIER L., JIER M., JOHNSTON L.,
RA JONES M., KERSHAW J., KIRSTEN J., LAISTER N., LATREILLE P.,
RA LIGHTNING J., LLOYD C., MCMURRAY A., MORTIMORE B., O'CALLAGHAN M.,
RA PARSONS J., PERCY C., RIFKEN L., ROOPRA A., SAUNDERS D., SHOWNKEEN R.,
RA SMALDON N., SMITH A., SONNHAMMER E., STADEN R., SULTON J.,
RA THERRY-MIEG J., THOMAS K., VAUDIN M., VAUGHAN K., WATERSTON R.,
RA WATSON A., WEINSTOCK L., WILKINSON-SPROAT J., WOHLDMAN P.;
RT "2.2 Mb of contiguous nucleotide sequence from chromosome III of C. elegans."

RL NATURE 368:32-38(1994).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN-BRISTOL N2;
 RA MAGGI L., GOELA D.;
 RL SUBMITTED (JAN-1998) TO EMBL/GENBANK/DBJ DATA BANKS.
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN-BRISTOL N2;
 RA WATERSTON R.;
 RL SUBMITTED (DEC-1997) TO EMBL/GENBANK/DBJ DATA BANKS.
 DR EMBL: AF040647; G2746830; -;
 SQ SEQUENCE 195 AA; 22009 MW; 8C0B0769 CRC32;

Query Match 100.0%; Score 41; DB 5; Length 195;
 Best Local Similarity 100.0%; Pred. No. 5.47e+01;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 138 NSFRY 142
 QY 1 NSFRY 5
 |||||

RESULT 7
 ID Q32561 PRELIMINARY; PRT; 513 AA.
 AC Q32561;
 DT 01-JAN-1998 (TREMBLREL. 05, CREATED)
 DT 01-JAN-1998 (TREMBLREL. 05, LAST SEQUENCE UPDATE)
 DT 01-AUG-1998 (TREMBLREL. 07, LAST ANNOTATION UPDATE)
 DE KETO ACID FORMATE-LYASE (FRAGMENT).
 GN TDCE.
 OS ESCHERICHIA COLI.
 OC BACTERIA; PROTEOBACTERIA; GAMMA SUBDIVISION; ENTEROBACTERIACEAE;
 OC ESCHERICHIA.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-W3110;
 RA HESSLINGER C., SAWERS G.;
 RL SUBMITTED (SEP-1997) TO EMBL/GENBANK/DBJ DATA BANKS.
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN-W3110;
 RA HESSLINGER C., FAIRHURST S.A., SAWERS G.;
 RL SUBMITTED (SEP-1997) TO EMBL/GENBANK/DBJ DATA BANKS.
 DR EMBL: AJ001620; E1169787; -;
 KW LYASE.
 FT NON-TER
 SQ SEQUENCE 513 AA; 58248 MW; A8023A3E CRC32;

Query Match 100.0%; Score 41; DB 2; Length 513;
 Best Local Similarity 100.0%; Pred. No. 5.47e+01;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 357 NSFRY 361
 QY 1 NSFRY 5
 |||||

RESULT 8
 ID Q64715 PRELIMINARY; PRT; 635 AA.
 AC Q64715;
 DT 01-AUG-1998 (TREMBLREL. 07, CREATED)
 DT 01-AUG-1998 (TREMBLREL. 07, LAST SEQUENCE UPDATE)
 DT 01-AUG-1998 (TREMBLREL. 07, LAST ANNOTATION UPDATE)
 DE T8K22.8 PROTEIN.
 GN T8K22.8.
 OS ARABIDOPSIS THALIANA (MOUSE-EAR CRESS).
 OC EUKARYOTA; VIRIDIPANTAE; STREPTOPHYTA;
 OC EUPHYLIOPHYTES; SPERMATOPHYTA; MAGNOLIOPHYTA; EUDICOTYLEDONS; ROSIDAE;
 OC CAPPARALES; BRASSICACEAE; ARABIDOPSIS.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=CV. COLUMBIA;

RA ROUNSLEY S.D., LIN X., KETCHUM K.A., CROSBY M.L., BRANDON R.C.,
 RA SYKES S.M., KAUL S., MASON T.M., KERLAVAGE A.R., ADAMS M.D.,
 RA SOMERVILLE C.R., VENTER J.C.;
 RL SUBMITTED (JUN-1998) TO EMBL/GENBANK/DBJ DATA BANKS.
 DR EMBL: AC004136; G3184278; -;
 SQ SEQUENCE 635 AA; 72049 MW; 07FC643C CRC32;

Query Match 100.0%; Score 41; DB 10; Length 635;
 Best Local Similarity 100.0%; Pred. No. 5.47e+01;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 439 NSFRY 443
 QY 1 NSFRY 5
 |||||

RESULT 9
 ID P91157 PRELIMINARY; PRT; 993 AA.
 AC P91157;
 DT 01-MAY-1997 (TREMBLREL. 03, CREATED)
 DT 01-MAY-1997 (TREMBLREL. 03, LAST SEQUENCE UPDATE)
 DT 01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)
 DE COSMID C44C3.
 GN C44C3.3.
 OS CAENORHABDITIS ELEGANS.
 OC EUKARYOTA; METAZOA; NEMATODA; SECERNENTEA; RHABDITIA; RHABDITIDA;
 OC RHABDITINA; RHABDITOIDEA; RHABDITIDAE; PELODERINAE; CAENORHABDITIS.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-BRISTOL N2;
 RX MEDLINE: 94150718.
 RA WILSON R., AINSKOUGH R., ANDERSON K., BAYNES C., BERKS M.,
 RA BONFIELD J., BURTON J., CONNELL M., COPSEY T., COOPER J., COULSON A.,
 RA CRAXTON M., DEAR S., DU Z., DURBIN R., FAVELLO A., FULTON L.,
 RA GARDNER A., GREEN P., HAWKINS T., HILLIER N., JIER M., JOHNSTON L.,
 RA JONES M., KERSHAW J., KIRSTEN J., LAISTER N., LATREILLE P.,
 RA LIGHTNING J., LLOYD C., McMURRAY A., MORTIMORE B., O'CALLAGHAN M.,
 RA PARSONS J., PERCY C., RIFKEN L., ROOPRA A., SAUNDERS D., SHOWNKEEN R.,
 RA SMALDON N., SMITH A., SONNHAMMER E., STADEN R., SULSTON J.,
 RA THIERRY-MIEG J., THOMAS K., VAUDIN M., VAUGHAN K., WATERSTON R.,
 RA WATSON A., WEINSTOCK L., WILKINSON-SPROAT J., WOHLDMAN P.;
 RT "2.2 Mb of contiguous nucleotide sequence from chromosome III of C.
 elegans".
 RL NATURE 368:32-38(1994).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN-BRISTOL N2;
 RA TIN A.;
 RL SUBMITTED (JAN-1997) TO EMBL/GENBANK/DBJ DATA BANKS.
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN-BRISTOL N2;
 RA WATERSTON R.;
 RL SUBMITTED (NOV-1996) TO EMBL/GENBANK/DBJ DATA BANKS.
 DR EMBL: U80028; G1699137; -;
 SQ SEQUENCE 993 AA; 115001 MW; A6FCFA5E CRC32;

Query Match 100.0%; Score 41; DB 5; Length 993;
 Best Local Similarity 100.0%; Pred. No. 5.47e+01;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 592 NSFRY 596
 QY 1 NSFRY 5
 |||||

RESULT 10
 ID Q56386 PRELIMINARY; PRT; 79 AA.
 AC Q56386;
 DT 01-NOV-1996 (TREMBLREL. 01, CREATED)
 DT 01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)
 DT 01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)
 DE HYPOTHETICAL 9.2 KD PROTEIN.

OS BACTEROIDES FRAGILIS.
 OC BACTERIA; CYTODHAGALES; BACTEROIDACEAE; BACTEROIDES.
 [1]
 RN SEQUENCE FROM N.A.
 RA TRANSPONSON-TRANSPONSON TN4351;
 RC RASMUSSEN J.L.;
 DR EMBL: 13049; ARATH: 2249.1.
 SQ SEQUENCE 141 AA; 16689 MW; 956EBE94 CRC32;
 [2]
 RN SEQUENCE FROM N.A.
 RC TRANSPONSON-TRANSPONSON TN4351;
 RX MEDLINE: 87279905.
 RA RASMUSSEN J.L.; ODELLSON D.A.; MACRINA F.L.;
 RT "Complete nucleotide sequence of insertion element IS4351 from
 Bacteroides fragilis."
 RL J. BACTERIOL. 169:3573-3580(1987).
 DR EMBL: M17124; G1197008;
 SQ SEQUENCE 79 AA; 9166 MW; 9E31B22F CRC32;

Query Match 95.1%; Score 39; DB 2; Length 79;
 Best Local Similarity 80.0%; Pred. No. 1.41e+02;
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Db 40 DSFRY 44
 :||||
 QY 1 NSFRY 5

RESULT 11
 ID Q58090 PRELIMINARY; PRT; 107 AA.
 AC Q58090;
 DT 01-AUG-1998 (TREMELREL. 07, CREATED)
 DT 01-AUG-1998 (TREMELREL. 07, LAST SEQUENCE UPDATE)
 DT 01-JAN-1999 (TREMELREL. 09, LAST ANNOTATION UPDATE)
 DE 107AA LONG HYPOTHETICAL PROTEIN.
 GN PHO352.
 OS PYROCOCUS HORIKOSHII.
 OC ARCHAEA; EUYARCHAEOTA; THERMOCOCCALES; THERMOCOCCACEAE; PYROCOCUS.
 [1]
 RN SEQUENCE FROM N.A.
 RC STRAIN-OT3;
 RX MEDLINE: 98344137.
 RA KAWARABAYASI Y.; SAWADA M.; HORIKAWA H.; HATAKAWA Y.; HINO Y.;
 RA YAMAMOTO S.; SEKINE M.; BABA S.; KOSUGI H.; HOSONUMA A.; NAGAI Y.;
 RA SAKAI M.; OGURA K.; OTUKA R.; NAKAZAWA H.; TAKAMIYA M.; OHFUKU Y.;
 RA FUNAHASHI T.; TANAKA T.; KUDOH Y.; YAMAZAKI J.; KUSHIDA N.; OGUCHI A.;
 RA AOKI K.; NAKAMURA Y.; ROBB T.F.; HORIKOSHI K.; MASUCHI Y.; SHIZUYA H.;
 RA KIKUCHI H.;
 RT "Complete Sequence and Gene Organization of the Genome of a
 Hyper-thermophilic Archaeobacterium, Pyrococcus horikoshii OT3."
 RL DNA RES. 5:55-76(1998).
 DR EMBL: AP000002; D1030369;
 SQ SEQUENCE 107 AA; 11348 MW; D4781A0C CRC32;

Query Match 95.1%; Score 39; DB 1; Length 107;
 Best Local Similarity 80.0%; Pred. No. 1.41e+02;
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Db 88 NAFRY 92
 :||||
 QY 1 NSFRY 5

RESULT 12
 ID P93305 PRELIMINARY; PRT; 141 AA.
 AC P93305;
 DT 01-MAY-1997 (TREMELREL. 03, CREATED)
 DT 01-MAY-1997 (TREMELREL. 03, LAST SEQUENCE UPDATE)
 DT 01-JAN-1999 (TREMELREL. 09, LAST ANNOTATION UPDATE)
 DE ORF141.
 OS ARABIDOPSIS THALIANA (MOUSE-EAR CRESS).
 OC EUKARYOTA; VIRIDIPANTAE; STREPTOPHYTA; EMBRYOPHYTA; TRACHEOPHYTA;
 OC EUPHYLLIPHYTES; SPERMATOPHYTA; MAGNOLIOPHYTA; EUDICOTYLEDONS; ROSIDAE;
 OC CAPPARALES; BRASSICACEAE; ARABIDOPSIS.

[1]
 RN SEQUENCE FROM N.A.
 RA UNSELD M.; MARIENFELD J.R.; BRANDT P.; BRENNICKE A.;
 RL NAT. GENET. 0:0-0(0).
 DR EMBL: Y08501; E283595;
 DR MENDEL; 13049; ARATH: 2249.1.
 SQ SEQUENCE 141 AA; 16689 MW; 956EBE94 CRC32;

Query Match 95.1%; Score 39; DB 10; Length 141;
 Best Local Similarity 80.0%; Pred. No. 1.41e+02;
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Db 84 DSFRY 88
 :||||
 QY 1 NSFRY 5

RESULT 13
 ID O77421 PRELIMINARY; PRT; 190 AA.
 AC O77421;
 DT 01-NOV-1998 (TREMELREL. 08, CREATED)
 DT 01-NOV-1998 (TREMELREL. 08, LAST SEQUENCE UPDATE)
 DT 01-NOV-1998 (TREMELREL. 08, LAST ANNOTATION UPDATE)
 DE FEMALE-SPECIFIC HISTAMINE-BINDING PROTEIN 2.
 OS RHIPICEPHALUS APPENDICULATUS.
 OC EUKARYOTA; METAZOA; ARTHROPODA; CHELICERATA; ARACHNIDA; ACARI;
 OC PARASITIFORMES; IXODIDA; IXODIDAE; RHIPICEPHALUS.
 [1]
 RN SEQUENCE FROM N.A.
 RC TISSUE-SALIVARY GLAND;
 RA PASEN G.C.; NUTTALL P.A.;
 RT "A family of histamine-binding salivary proteins from the brown ear
 tick, Rhipicephalus appendiculatus."
 RL SUBMITTED (APR-1997) TO EMBL/GENBANK/DBJ DATA BANKS.
 DR EMBL: U96081; G3452089;
 SQ SEQUENCE 190 AA; 21464 MW; 08168E2F CRC32;

Query Match 95.1%; Score 39; DB 5; Length 190;
 Best Local Similarity 80.0%; Pred. No. 1.41e+02;
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Db 115 NAFRY 119
 :||||
 QY 1 NSFRY 5

RESULT 14
 ID O12300 PRELIMINARY; PRT; 209 AA.
 AC O12300;
 DT 01-JUL-1997 (TREMELREL. 04, CREATED)
 DT 01-JUL-1997 (TREMELREL. 04, LAST SEQUENCE UPDATE)
 DT 01-NOV-1998 (TREMELREL. 08, LAST ANNOTATION UPDATE)
 DE REPLICASE.
 OS GALINSOGA MOSAIC CARMOVIRUS.
 OC VIRUSES; SSRNA POSITIVE-STRAND VIRUSES, NO DNA STAGE; TOMBUSVIRIDAE;
 OC CARMOVIRUS.
 [1]
 RN SEQUENCE FROM N.A.
 RX MEDLINE: 98166875.
 RA CIUFFREDA P.; RUBINO L.; RUSSO M.;
 RT "Molecular cloning and complete nucleotide sequence of galinsoga
 mosaic virus genomic RNA."
 RL ARCH. VIROL. 143:173-190(1998).
 [2]
 RN SEQUENCE FROM N.A.
 RA RUSSO M.;
 RL SUBMITTED (MAY-1997) TO EMBL/GENBANK/DBJ DATA BANKS.
 DR EMBL: Y13463; E321113;
 SQ SEQUENCE 209 AA; 22949 MW; 4D31DD75 CRC32;

Query Match 95.1%; Score 39; DB 14; Length 209;
 Best Local Similarity 80.0%; Pred. No. 1.41e+02;
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Db 29 NAFRY 33
I:||||
Qy 1 NSFry 5

RESULT 15
ID O31875 PRELIMINARY; PRT: 240 AA.
AC O31875;
DT 01-JAN-1998 (TREMBREL. 05, CREATED)
DT 01-JAN-1998 (TREMBREL. 05, LAST SEQUENCE UPDATE)
DT 01-NOV-1998 (TREMBREL. 08, LAST ANNOTATION UPDATE)
DE YOSN PROTEIN.
GN YOSN.
OS BACILLUS SUBTILIS.
OC BACTERIA; FIRMICUTES; BACILLUS/CLOSTRIDIUM GROUP; BACILLACEAE;
OC BACILLUS.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-168;
RX MEDLINE: 98044033.
RA KUNST F., OGASAWARA N., MOSZER I., ALBERTINI A.M., ALLONI G.,
RA AZEVEDO V., BERTERO M.G., BESSIERES P., BOLOTIN A., BORCHERT S.,
RA BORRIS R., BOURSIER L., BRANS A., BRAUN M., BRIGNELL S.C., BRON S.,
RA BROUILLET S., BRUSCHI C.V., CALDWELL B., CAPUANO V., CARTER N.M.,
RA CHOI S.K., CODANI J.J., CONNERTON I.F., CUMMINGS N.J., DANIEL R.A.,
RA DENIZOT F., DEVINE K.M., DUSTERHOFT A., EHRLICH S.D., EMMERSON P.T.,
RA ENTIAN K.D., ERRINGTON J., FABRET C., FERRARI E., FOULGER D.,
RA FRITZ C., FUJITA M., FUJITA Y., FUMA S., GALIZZI A., GALLERON N.,
RA GHM S.Y., GLASER P., GOFFEAU A., GOLIGHTLY E.J., GRANDI G.,
RA GUSEPPI G., GUY B.J., HAGA K., HAECH J., HARWOOD C.R., HENAUT A.,
RA HILBERT H., HOLSAPPEL S., HOSONO S., HULLO M.F., ITAYA M., JONES L.,
RA JORIS B., KARAHARA D., KASAHARA Y., KLAER-BLANCHARD M., KLEIN C.,
RA KOBAYASHI Y., KOTTER P., KONINGSTEIN G., KROGH S., KUMANO M.,
RA KURITA K., LAPIDUS A., LARDINOIS S., LAUBER J., LAZAREVIC V.,
RA LEE S.M., LEVINE A., LIU H., MASUDA S., MAUEL C., MEDIGUE C.,
RA MEDINA N., MELLADO R.P., MIZUNO M., MOESTL D., NAKAI S., NOBACK M.,
RA NOONE D., O'REILLY M., OGAWA K., OGIWARA A., OUDEGA B., PARK S.H.,
RA PARRO V., POHL T.M., PORTETELLE D., PORNOLLIK S., PRESCOTT A.M.,
RA PRESECAN E., PUJIC P., PURNELLE B., RAPOPORT G., REY M., REYNOLDS S.,
RA RIEGER M., RIVOLTA C., ROCHA E., ROCHE B., ROSE M., SADAIE Y.,
RA SATO T., SCANLAN E., SCHLEICH S., SCHROETER R., SCOFFONE F.,
RA SERIGUCHI J., SEROWSKA A., SEROR S.J., SERROR P., SHIN B.S., SOLDI B.,
RA SOROKIN A., TACCONI E., TAKAGI T., TAKAHASHI H., TAKEMARU K.,
RA TAKEUCHI M., TAMAKOSHI A., TANAKA T., TERPSTRA P., TOGNONI A.,
RA TOSATO V., UCHIYAMA S., VANDENBOL M., VANNIER F., VASSAROTTI A.,
RA VIARI A., WAMBUTT R., WEDLER E., WEDLER H., WEITZENEGGER T.,
RA WINTERS P., WIPAT A., YAMAMOTO H., YAMANE K., YASUMOTO K., YATA K.,
RA YOSHIDA K., YOSHIKAWA H.F., ZUMSTEIN E., YOSHIKAWA H., DANCHIN A.,
RT "The complete genome sequence of the gram-positive bacterium Bacillus
RT subtilis.";
RL NATURE 390:249-256(1997).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN-168;
RA KUNST F., OGASAWARA N., YOSHIKAWA H., DANCHIN A.;
RL SUBMITTED (NOV-1997) TO EMBL/GENBANK/DDBJ DATA BANKS.
DR EMBL: Z99114; E1185478; .
DR PFAM: PF00317; ribonucleoired; 1.
SQ SEQUENCE 240 AA; 27966 MW; 16160EDD CRC32;

Query Match 95.18; Score 39; DB 2; Length 240;
Best Local Similarity 80.0%; Pred. No. 1.41e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Db 231 NAFRY 235
I:||||
Qy 1 NSFry 5

Search completed: Wed Jun 16 13:24:43 1999
Job time : 34 secs.

MPSRCH_PP
(TM)

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MPSRCH_PP protein - protein database search, using Smith-Waterman algorithm

Run on: Wed Jun 16 12:47:54 1999; MasPar time 4.58 Seconds
171.977 Million cell updates/sec

Tabular output not generated.

Title: >VANDER-027-213.PEP

Description: (1-37) from vander0277777.ppe

Perfect Score: 279
Sequence: 1 LRALLTAPRSLRRSSFCGRMDRIGAGSLGNSFRY 37

Scoring table: PAM 150
Gap 11

Searched: 170751 seqs, 21266608 residues

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database: a-geneseq35
1:part1 2:part2 3:part3 4:part4 5:part5 6:part6 7:part7
8:part8 9:part9 10:part10 11:part11 12:part12 13:part13
14:part14 15:part15 16:part16 17:part17 18:part18
19:part19 20:part20 21:part21 22:part22 23:part23
24:part24 25:part25 26:part26 27:part27 28:part28
29:part29 30:part30 31:part31 32:part32 33:part33
34:part34 35:part35 36:part36 37:part37 38:part38
39:part39

Statistics: Mean 24.237; Variance 85.878; scale 0.282

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description	Pred. No.
1	279	100.0	88	3 P50493	Cardioidilatin peptide	2.60e-21
2	279	100.0	126	27 W34533	Human atrial natriuretic	2.60e-21
3	279	100.0	126	4 P51240	Sequence of pro-atria	2.60e-21
4	279	100.0	126	3 P50037	Sequence of human gam	2.60e-21
5	279	100.0	126	2 R00582	Human gamma atrial na	2.60e-21
6	279	100.0	136	7 R36935	Human pre-proANVP #2	2.60e-21
7	279	100.0	147	1 R03301	Sequence of pre-human	2.60e-21
8	279	100.0	151	7 R36934	Human pre-proANVP #1	2.60e-21
9	279	100.0	151	3 P50036	Sequence of the precu	2.60e-21
10	279	100.0	151	3 P50050	Cardioidilatin peptide	2.60e-21
11	275	98.6	151	2 P70629	Sequence encoded by h	7.39e-21
12	267	95.7	125	1 P82656	Vasodilatory peptide	5.96e-20
13	267	95.7	150	4 P51239	Sequence of pre-pro-a	5.96e-20
14	267	95.7	150	4 P51241	Sequence of pre-pro-a	5.96e-20
15	264	94.6	48	3 P50115	Rat atrial natriureti	1.30e-19
16	264	94.6	62	3 P60165	Rat recombinant pro-c	1.30e-19

17	264	94.6	71	4 P51102	Sequence of peptide(s	1.30e-19
18	264	94.6	73	4 P51107	Sequence of atrial na	1.30e-19
19	264	94.6	111	3 P50565	Sequence of polypepti	1.30e-19
20	264	94.6	126	3 P60017	Sequence of cardionat	1.30e-19
21	264	94.6	128	4 P51238	Sequence of pro-atria	1.30e-19
22	264	94.6	152	2 P60325	Ggamma-rat atrial nat	1.30e-19
23	264	94.6	152	7 R36936	Rat pre-proANVP	1.30e-19
24	264	94.6	152	4 P51242	Sequence of pre-pro-a	1.30e-19
25	262	93.9	116	3 P50102	Atrial natriuretic fa	2.19e-18
26	252	90.3	144	4 R21676	Beta-gal leader and p	2.95e-18
27	252	90.3	144	4 R21677	Beta-gal leader and p	2.95e-18
28	250	89.6	35	1 R06353	Atrial natriuretic fa	4.95e-18
29	244	87.5	35	3 P50112	Biologically active s	2.34e-17
30	244	87.5	35	2 R08328	Chelated atrial natri	2.34e-17
31	242	86.7	32	2 P80388	Sequence of new biolo	3.93e-17
32	242	86.7	32	36 W67039	Atrial natriuretic pe	3.93e-17
33	242	86.7	32	17 R88516	Urodilatin, a biologi	3.93e-17
34	242	86.7	40	25 W21945	Fusion protein compri	3.93e-17
35	242	86.7	40	25 W33021	Fusion protein compri	3.93e-17
36	235	84.2	33	4 P51103	Sequence of atrial na	2.39e-16
37	235	84.2	35	1 R06352	Atrial natriuretic fa	2.39e-16
38	235	84.2	35	2 R08327	Chelated atrial natri	2.39e-16
39	234	83.9	35	3 P61765	Sequence of peptide h	3.09e-16
40	234	83.9	151	4 P51237	Sequence of pre-pro-a	3.09e-16
41	233	83.5	35	3 P60806	Atrial natriuretic fa	4.00e-16
42	231	82.8	35	3 P60270	Sequence of peptide h	6.70e-16
43	229	82.1	152	2 P81655	Sequence encoded by p	1.12e-15
44	227	81.4	32	4 P51104	Sequence of atrial na	1.87e-15
45	225	80.6	31	2 P71465	Sequence of aldostero	3.13e-15

ALIGNMENTS

RESULT 1
ID P50493 standard; protein; 88 AA.

AC P50493;
DT 18-MAR-1992 (first entry)
DE Cardioidilatin peptide hormone variant.
KW Cardioidilatin; peptide; hormone; hypotensive; ss.
PN W08502850-A.
PD 04-JUL-1985.
PF 21-DEC-1984; D00279.
PR 24-DEC-1983; DE-346953.
PA (ORGA-) ORGANOGEN MED MOL.
PI Forssmann WG;
DR WPI; 85-171361/28.

PT New peptide hormone cardioidilatin - from atrium tissue having
PT effects on heart muscle ionotropy, smooth muscle, and sweat
secretion

PS Claim 22; Page 16; 35pp; German.

CC This variant of the peptide described in P50491 has a mol.wt.
of 13,000 and an isoelectric point of 6-6.5. This peptide
hormone, as well as its C-terminal fragments obtained by
partial bronchov separation between the Met groups and
behind the latter, has strong relaxation activity on smooth
vasomuscles. It also affects sweat secretion and can be used for
the diagnosis and therapy of hypertension. It can also be used for
the treatment of post-operative cardiovascular disorders, skin
diseases, etc. The hormone may be prepared from a heart atrium
extract. See also P50491-2.
CC Sequence 88 AA;

Query Match 100.0%; Score 279; DB 3; Length 88;
Best Local Similarity 100.0%; Pred. No. 2.60e-21;
Matches 37; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 52 lralltapsrlrrssfcgrmdrigragslqgnsfry 88
|||||

QY 1 LRALLTAPRSLRRSSFCGRMDRIGAGSLGNSFRY 37
|||||

RESULT 2
ID W34533 standard; Protein; 126 AA.

AC W34533;
 DT 24-MAR-1998 (first entry)
 DE Human atrial natriuretic factor prohormone.
 KW Human atrial natriuretic factor prohormone; therapy; hypertension;
 KW congestive heart failure; pulmonary oedema; toxemia of pregnancy;
 KW nephrotic syndrome; renal failure; hepatic cirrhosis; hyperkalemia;
 KW acidosis; digitalis overdose; insulin deficiency; Addison's disease;
 KW proANF; hyperaldosteronism.
 OS Homo sapiens.
 PN US5691310-A.
 PD 25-NOV-1997.
 PF 09-MAR-1995; 401246.
 PR 09-MAR-1995; US-401246.
 PR 29-SEP-1987; US-102477.
 PR 01-MAY-1990; US-517252.
 PR 14-NOV-1991; US-799211.
 PA (VESELY) VESELY D L.
 PI Vesely DL;
 DR WPI: 98-017684/02.
 DT Treatment of hypertension and related disorders - with synthetic
 FT peptide fragment of atrial natriuretic factor prohormone
 PS Disclosure; Column 4; 19pp; English.
 CC This sequence represents the human atrial natriuretic factor prohormone
 CC (proANF). Fragments of this sequence (see W34521-W34523) can be used in
 CC the method of the invention. The method is for treating hypertension,
 CC congestive heart failure, pulmonary oedema, toxemia of pregnancy,
 CC nephrotic syndrome, acute and chronic renal failure or hepatic cirrhosis
 CC with or without ascites comprises administering a synthetic peptide
 CC consisting of amino acids 1-30, 31-67 or 79-98 of proANF. The peptides
 CC proANF(1-30) and proANF(79-98) can also be used in a method for treating
 CC hyperkalemia associated with acidosis, digitalis overdose,
 CC succinylcholine, insulin deficiency, acute or chronic renal failure,
 CC Addison's disease or hyperaldosteronism. The peptides have hypertensive,
 CC diuretic, natriuretic and/or kalluretic activity.
 SQ Sequence 126 AA;

Query Match 100.0%; Score 279; DB 27; Length 126;
 Best Local Similarity 100.0%; Pred. No. 2.60e-21;
 Matches 37; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Db 90 lralltaprslrrscfgrmdrigagsglgnsfry 126
 |||||
 QY 1 LRALLTAPRSLRRSCFGRMDRIGAGSGLGCSNFRY 37

RESULT 3
 ID P51240 standard; peptide; 126 AA.
 AC P51240;
 DT 03-AUG-1992 (first entry)
 DE Sequence of pro-atrial natriuretic/vasodilator polypeptide
 DE (ANVP).
 KW Natriuretic; diuretic; vasodilator;
 KW renin-angiotensin-aldosterone-system.
 OS Mammal.
 FH Key Location/Qualifiers
 FT modified_site 1
 FT /label= H-M
 FT disulfide_bond 105..121
 FT modified_site 126
 FT /label= Y-OH
 FT W08504870-A.
 PD 07-NOV-1985.
 PF 16-APR-1985; U00658.
 PR 19-APR-1984; US-602117.
 PR 01-JUN-1984; US-616488.
 PR 20-JUN-1984; US-622839.
 PA (BIOT-) BIOTECHNOL RES PART.
 PI Johnson LK, Atlas SA, McCarthy BJ, Larragh JH, Lewicki JA;
 DR WPI: 85-289654/46.
 DT New atrial polypeptide cpds. - useful as natriuretics,
 FT diuretics, vasodilators and modulators of the
 FT renin-angiotensin-aldosterone system
 PS Claim 8; Page 116; 144pp; English.

CC The inventors claim a polypeptide comprising atrial natriuretic/
 CC vasodilator polypeptide (ANVP), pro-ANVP or pre-pro-ANVP, or their
 CC fragments. The encoding DNA sequence is also claimed. The claimed
 CC polypeptides are natriuretics, diuretics, vasodilators and
 CC modulators of the renin-angiotensin-aldosterone system. Dose is
 CC 0.01-100 ug/kg.
 SQ Sequence 126 AA;

Query Match 100.0%; Score 279; DB 4; Length 126;
 Best Local Similarity 100.0%; Pred. No. 2.60e-21;
 Matches 37; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 90 lralltaprslrrscfgrmdrigagsglgnsfry 126
 |||||
 QY 1 LRALLTAPRSLRRSCFGRMDRIGAGSGLGCSNFRY 37

RESULT 4
 ID P50037 standard; Protein; 126 AA.
 AC P50037;
 DT 03-SEP-1991 (first entry)
 DE Sequence of human gamma-atrium natriuretic polypeptide (ANP).
 KW Natriuretic; diuretic; hypotensive; antihypertensive.
 OS Homo sapiens.
 PN EP-164273-A.
 PD 11-DEC-1985.
 PF 08-JUN-1984; 116605.
 PR 08-JUN-1984; JP-116606.
 PR 08-JUN-1984; JP-116605.
 PA (SUNR) SUNTORY LTD.
 PI Matsuo H, Kangawa K, Hayashi Y, Oikawa S, Oshima T,
 PI Tanaka S, Nakazato H, Tawaragi Y;
 DR WPI: 85-312162/50.
 DR N-PSDB: N50055.
 PT New DNA sequences from human atrium cordis - coding for new
 PT diuretic polypeptide or precursor cpds.
 PS Claim 26; Page 37; 53pp; English.
 CC The precursor of human gamma-ANP and its 26Asn-151tyr fragmentare
 CC claimed (P50036, P50037), as are the DNA SQs encoding them (N50020,
 CC N50055). The 26Asn-151tyr fragment has a diuretic action so is
 CC useful as a hypotensive/antihypertensive agent. The usual dose is 0.
 CC 01-1 mg/kg.
 SQ Sequence 126 AA;

Query Match 100.0%; Score 279; DB 3; Length 126;
 Best Local Similarity 100.0%; Pred. No. 2.60e-21;
 Matches 37; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 90 lralltaprslrrscfgrmdrigagsglgnsfry 126
 |||||
 QY 1 LRALLTAPRSLRRSCFGRMDRIGAGSGLGCSNFRY 37

RESULT 5
 ID R00582 standard; protein; 126 AA.
 AC R00582;
 DT 05-JUN-1989 (first entry)
 DE Human gamma atrial natriuretic polypeptide (gamma-hANP).
 KW Gamma atrial natriuretic polypeptide; ANP; natriuretic;
 KW hypertension; cirrhosis; nephrosis; heart disease.
 OS Homo sapiens.
 PN EP-350227-A.
 PD 10-JAN-1988.
 PF 30-JUN-1989; 306669.
 PR 04-JUL-1988; JP-166641.
 PA (SHIO) Shionogi Selyaku Kabushiki.
 PI Imura H, Nakao K;
 DR WPI: 90-009970/02.
 DT Monoclonal antibodies recognising gamma-atrial natriuretic -
 PT used for diagnosis of diseases eg kidney and heart disease.
 PS Disclosure; Fig.1; 10pp; English.
 CC Gamma-hANP of which the N-terminal 25 AAs are recognisyl monoclonal
 CC antibodies of the invention

SQ Sequence 126 AA;

Query Match 100.0%; Score 279; DB 2; Length 126;
Best Local Similarity 100.0%; Pred. No. 2.60e-21;
Matches 37; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 90 lraltapslrsscfgrmdrigagsglgnsfry 126
|||||
Qy 1 LRALLTAPSLRSSCFGRMDRIGAGSGLGNCSFRY 37

RESULT 6

ID R36935 standard; Protein; 136 AA.
AC R36935;
DT 14-SEP-1993 (first entry)
DE Human pre-proANVP #2.
KW Human; pre-pro; atrial natriuretic/vasodilator peptide; ANVP; rat;
KW regulation; fluid volume; blood pressure.
OS Homo sapiens.
PN US212286-A.
PD 18-MAY-1993.
PF 09-APR-1984; 602117.
PF 09-APR-1984; US-602117.
PR 01-JUN-1984; US-616488.
PR 08-MAY-1985; US-766030.
PR 05-JUN-1986; US-870795.
PA (SCIO-) SCIOS NOVA INC.
PI Lewicki JA, Scarborough RM;
DR WPI; 93-175525/21.
DR N-PSDB; 041455.
PT New polypeptide cpd. - useful as natriuretic, diuretic and/or
PT vasodilator in mammals
PS Disclosure; Fig 1B; 45pp; English.
CC This sequence is encoded by the human pre-pro atrial natriuretic/
CC vasodilator peptide (ANVP) cDNA. Fragments of this protein and the
CC corresponding sequence in rat (see also R36936), may be used for
CC regulation of fluid volume and blood pressure in host organisms.
CC The ANVP fragments may be produced by solid-phase techniques. See
CC also R36937-78.
SQ Sequence 136 AA;

Query Match 100.0%; Score 279; DB 7; Length 136;
Best Local Similarity 100.0%; Pred. No. 2.60e-21;
Matches 37; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 100 lraltapslrsscfgrmdrigagsglgnsfry 136
|||||
Qy 1 LRALLTAPSLRSSCFGRMDRIGAGSGLGNCSFRY 37

RESULT 7

ID R03301 standard; protein; 147 AA.
AC R03301;
DT 15-AUG-1990 (first entry)
DE Sequence of pre-human atrial natriuretic peptide.
KW Human-chAMP; diuretic; antihypertensive; ss.
OS Homo sapiens.
PN J02025499-A.
PD 26-JAN-1990.
PF 14-JUL-1988; 173739.
PR 14-JUL-1988; JP-173739.
PA (MATSUO) Matsuo T.
PI WPI; 90-071804/10.
PT Physio-active peptide derived from birds - has cysteine bridge.
PT specified AA sequence and diuretic and antihypertensive properties.
PS Disclosure; Fig 14; 16pp; Japanese.
CC This sequence has 99 amino acid residues homologous to the pre-chAMP.
CC See also Q03466-Q03468, R03301 and R03402.
SQ Sequence 147 AA;

Query Match 100.0%; Score 279; DB 1; Length 147;
Best Local Similarity 100.0%; Pred. No. 2.60e-21;
Matches 37; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 111 lraltapslrsscfgrmdrigagsglgnsfry 147
|||||
Qy 1 LRALLTAPSLRSSCFGRMDRIGAGSGLGNCSFRY 37

RESULT 8

ID R36934 standard; Protein; 151 AA.
AC R36934;
DT 14-SEP-1993 (first entry)
DE Human pre-proANVP #1.
KW Human; pre-pro; atrial natriuretic/vasodilator peptide; ANVP; rat;
KW regulation; fluid volume; blood pressure.
OS Homo sapiens.
PH Key Location/Qualifiers
FT peptide 1..41
FT /note= "Signal peptide"
FT protein 42..151
FT /note= "Mature protein"
PN US212286-A.
PD 18-MAY-1993.
PF 09-APR-1984; 602117.
PF 09-APR-1984; US-602117.
PR 01-JUN-1984; US-616488.
PR 08-MAY-1985; US-766030.
PR 05-JUN-1986; US-870795.
PA (SCIO-) SCIOS NOVA INC.
PI Lewicki JA, Scarborough RM;
DR WPI; 93-175525/21.
DR N-PSDB; 041454.
PT New polypeptide cpd. - useful as natriuretic, diuretic and/or
PT vasodilator in mammals
PS Disclosure; Fig 1A; 45pp; English.
CC This sequence is encoded by the human pre-pro atrial natriuretic/
CC vasodilator peptide (ANVP) DNA. Fragments of this protein and the
CC corresponding sequence in rat (see also R36936), may be used for
CC regulation of fluid volume and blood pressure in host organisms.
CC The ANVP fragments may be produced by solid-phase techniques. See
CC also R36937-78.
SQ Sequence 151 AA;

Query Match 100.0%; Score 279; DB 7; Length 151;
Best Local Similarity 100.0%; Pred. No. 2.60e-21;
Matches 37; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 115 lraltapslrsscfgrmdrigagsglgnsfry 151
|||||
Qy 1 LRALLTAPSLRSSCFGRMDRIGAGSGLGNCSFRY 37

RESULT 9

ID P50036 standard; Protein; 151 AA.
AC P50036;
DT 03-SEP-1991 (first entry)
DE Sequence of the precursor of human gamma-atrium natriuretic
DE polypeptide (ANP).
KW Natriuretic; diuretic; hypotensive; antihypertensive.
OS Homo sapiens.
PN EP-164273-A.
PD 11-DEC-1985.
PF 08-JUN-1984; 116605.
PR 08-JUN-1984; JP-116606.
PR 08-JUN-1984; JP-116605.
PA (SUNR) SUNTORY LTD.
PI Matsuo H, Kangawa K, Hayashi Y, Oikawa S, Oshima T,
PI Tanaka S, Nakazato H, Tawaragi Y;
DR WPI; 85-312162/50.
DR N-PSDB; N50020.
PT New DNA sequences from human atrium cordis - coding for new
PT diuretic polypeptide or precursor cpds.
PS Claim 25; Fig 5; 53pp; English.
CC The precursor of human gamma-ANP and its 26asn-151tyr fragmentare
CC claimed (P50036, P50037), as are the DNA SQs encoding them (N50020,

CC N50055). The 26asn-151tyr fragment has a diuretic action so is
CC useful as a hypotensive/antihypertensive agent. The usual dose is 0.
CC 01-1 mg/kg.
SQ Sequence 151 AA;

Query Match 100.0%; Score 279; DB 3; Length 151;
Best Local Similarity 100.0%; Pred. No. 2.60e-21;
Matches 37; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 115 lralltaprrlrrscfgrmdrigaegslgcnfsr 151
|||||
QY 1 LRALLTAPRSLRRSSCFGRMDRIGAQSGLGCSFRY 37

RESULT 10

ID P50050 standard; protein; 151 AA.
AC P50050;
DT 28-OCT-1991 (first entry)
DE Cardiodilatin peptide.
KW Cardiodilatin; plasmid PHANF48; muscle relaxant; antihypertensive.
OS Homo sapiens.
PN EP-159943-A.
PD 30-OCT-1985.
PF 11-APR-1985; 400726.
PR 12-APR-1984; JP-073663.
PR 21-JUN-1984; JP-128335.
PR 16-AUG-1984; JP-170739.
PR 12-OCT-1984; JP-213897.
PA (MITU) Mitsubishi Chemical Industries Ltd.
PI Nakanishi S, Teranishi Y, Nagahari K, Shibui T, Takamatsu K;
DR WPI; 85-271495/44.
DR N-PSDB; N50069.
PT Expression vector contg. gene for cardionatrin or cardiodilatin - and
PT corresp. DNA sequences, useful as antihypertensive agents.
PS Disclosure; Fig. 13; 45pp; English.
CC The DNA encoding the cardiodilatin is carried on plasmid PHANF48.
CC Cardiodilatin is a muscle relaxant, so is useful as an antihypertensive
CC agent. The DNA is obtd. from RNA isolated from the human heart.
SQ Sequence 151 AA;

Query Match 100.0%; Score 279; DB 3; Length 151;
Best Local Similarity 100.0%; Pred. No. 2.60e-21;
Matches 37; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 115 lralltaprrlrrscfgrmdrigaegslgcnfsr 151
|||||
QY 1 LRALLTAPRSLRRSSCFGRMDRIGAQSGLGCSFRY 37

RESULT 11

ID P70629 standard; protein; 151 AA.
AC P70629;
DT 09-APR-1991 (first entry)
DE Sequence encoded by human atrial natriuretic peptide factor (ANF)
DE gene.
KW DNA fingerprinting; probe; hypertension.
OS Homo sapiens.
PN W08702709-A.
PD 07-MAY-1987.
PF 24-OCT-1986; U02293.
PR 24-OCT-1985; US-790813.
PR 12-NOV-1985; US-796904.
PR 09-JAN-1986; US-817433.
PR 11-JUN-1986; US-873199.
PA (BIOT-) BIOTECHN RES PARTN.
PI Shine J, Baker AR, Frossard PM;
DR WPI; 87-136035/19.
DR N-PSDB; N70974.
PT Genetic analysis diagnostic for hypertension - by detecting
PT polymorphous of the renin, kallikrein or ANF gene regions
PS disclosure; Fig 2; 51pp; English.
CC The patent application is for a method used for determ. of a
CC genetic fingerprint of a subject which allows early diagnosis of

CC individuals at risk of hypertension and permits early therapeutic
CC measures to prevent the fatal symptomology of the disease. The
CC section of the genome which is fingerprinted or otherwise subject to
CC study using the results is dependent on the nature of the probe.
CC The probes useful in the present invention are selected from the
CC renin, kallikrein, or ANF gene (see FT).
SQ Sequence 151 AA;

Query Match 98.6%; Score 275; DB 2; Length 151;
Best Local Similarity 97.3%; Pred. No. 7.39e-21;
Matches 36; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Db 115 lralltaprrlrrscfgrmdrigaegslgcnfsr 151
|||||
QY 1 LRALLTAPRSLRRSSCFGRMDRIGAQSGLGCSFRY 37

RESULT 12

ID P82656 standard; protein; 125 AA.
AC P82656;
DT 16-NOV-1990 (first entry)
DE Vasodilatory peptide.
KW vasodilatory peptide; cardionatrin.
OS synthetic.
PN J63107997-A.
PD 12-MAY-1988.
PF 18-SEP-1986; 220835.
PR 18-SEP-1986; JP-220835.
PA (MITU) Mitsubishi Chem Ind KK.
DR WPI; 88-170991/25.
PT Biologically prepared peptide -
PT has vein relaxation activity.
PS Claim 1; page 1; 13pp; Japanese
CC This sequence was isolated from a cDNA library prepared from
CC poly(A) mRNA isolated from human heart. Sequences complementary
CC to the DNA encoding MDRIG of cardionatrin were isolated using
CC a mixture of oligonucleotide probes. Two plasmids, pH4VD and pHMANF,
CC identified by this screening process, were then used to transform
CC E.coli which were cultured to produce the peptide.
SQ Sequence 125 AA;

Query Match 95.7%; Score 267; DB 1; Length 125;
Best Local Similarity 100.0%; Pred. No. 5.96e-20;
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 90 lralltaprrlrrscfgrmdrigaegslgcnfsr 125
|||||
QY 1 LRALLTAPRSLRRSSCFGRMDRIGAQSGLGCSFR 36

RESULT 13

ID P51239 standard; peptide; 150 AA.
AC P51239;
DT 03-AUG-1992 (first entry)
DE Sequence of pre-pro-atrial natriuretic/vasodilator polypeptide
DE (ANVP).
KW Natriuretic; diuretic; vasodilator;
KW venin-angiotensin-aldosterone-system.
OS Mammal.
FH Key
FT modified_site 1 Location/Qualifiers
FT disulfide_bond 130...146 /label= H-M
FT modified_site 151 /label= Y-OH
FT W08504870-A.
PN PD 07-NOV-1985.
PF 16-APR-1985; U00658.
PR 19-APR-1984; US-802117.
PR 01-JUN-1984; US-816488.
PR 20-JUN-1984; US-622639.
PA (BIOT-) BIOTECHNOL RES PART.
PI Johnson LK, Atlas SA, McCarthy BJ, Laragh JH, Lewicki JA;

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DR WPI; 85-289654/46.
PT New atrial polypeptide cpds. - useful as natriuretics,
PT diuretics, vasodilators and modulators of the
PT renin-angiotensin-aldosterone system
PS Claim 7; Page 115; 144pp; English.
CC The inventors claim a polypeptide comprising atrial natriuretic/
CC vasodilator polypeptide (ANVP), pro-ANVP or pre-pro-ANVP, or their
CC fragments. The encoding DNA sequence is also claimed. The claimed
CC polypeptides are natriuretics, diuretics, vasodilators and
CC modulators of the renin-angiotensin-aldosterone system. Dose is
CC 0.01-100 ug/kg.
SQ Sequence 150 AA;

Query Match 95.7%; Score 267; DB 4; Length 150;
Best Local Similarity 100.0%; Pred. No. 5.96e-20;
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 115 lralltaprslrrscfgrmdrigagsglgnscfr 150
Qy 1 LRALLTAPRSLRRSSCFGRMDRIGAGSGLGNCNSFR 36

RESULT 14
ID P51241 standard; peptide; 150 AA.
AC P51241;
DT 03-AUG-1992 (first entry)
DE Sequence of pre-pro-atrial natriuretic/vasodilator
DE polypeptide (ANVP).
DE Natriuretic; diuretic; vasodilator;
KW venin-angiotensin-aldosterone-system.
OS Homo sapiens.
FH Key Location/Qualifiers
FT misc_difference 16..41
FT /note= "encoded by N50763"
PN W08504870-A.
PD 07-NOV-1985.
PF 16-APR-1985; U00658.
PR 19-APR-1984; US-602117.
PR 01-JUN-1984; US-616488.
PR 20-JUN-1984; US-622639.
PA (BIOT-) BIOTECHNOL RES PART.
PI Johnson LK, Atlas SA, McCarthy BJ, Laragh JH, Lewicki JA;
DR WPI; 85-289654/46.
DR N-PSDB; N50695; N50763.
PT New atrial polypeptide cpds. - useful as natriuretics,
PT diuretics, vasodilators and modulators of the
PT renin-angiotensin-aldosterone system
PS Example; Fig 1A; 144pp; English.
CC The inventors claim a polypeptide comprising atrial natriuretic/
CC vasodilator polypeptide (ANVP), pro-ANVP or pre-pro-ANVP, or their
CC fragments. The encoding DNA sequence is also claimed. The claimed
CC polypeptides are natriuretics, diuretics, vasodilators and
CC modulators of the renin-angiotensin-aldosterone system. Dose is
CC 0.01-100 ug/kg.
SQ Sequence 150 AA;

Query Match 95.7%; Score 267; DB 4; Length 150;
Best Local Similarity 100.0%; Pred. No. 5.96e-20;
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 115 lralltaprslrrscfgrmdrigagsglgnscfr 150
Qy 1 LRALLTAPRSLRRSSCFGRMDRIGAGSGLGNCNSFR 36

RESULT 15
ID P50115 standard; peptide; 48 AA.
AC P50115;
DT 22-OCT-1991 (first entry)
DE Rat atrial natriuretic factor-beta.
KW Atrial natriuretic factor; diuretic; hypotensive.
OS Rattus rattus.
FH Key Location/Qualifiers

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FT disulfide_bond 27..43
PN EP-153865-A.
PD 04-SEP-1985.
PF 28-FEB-1985; 301364.
PR 02-MAR-1984; JP-038816.
PA (SUNR ) SUNTORY LTD.
PI Matsuo H, Kangawa K;
DR WPI; 85-218348/36.
PT New diuretic, antihypertensive polypeptide - isolated from rat
PT atrium cordis.
PS Claim 1; Page 17; 23pp; English.
CC The rat atrial natriuretic factor-beta has diuretic, natriuretic and
CC hypotensive or hypertensive activity.
SQ Sequence 43 AA;

Query Match 94.6%; Score 264; DB 3; Length 48;
Best Local Similarity 91.9%; Pred. No. 1.30e-19;
Matches 34; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Db 12 lraltagprslrrscfgrmdrigagsglgnscfr 48
Qy 1 LRALLTAPRSLRRSSCFGRMDRIGAGSGLGNCNSFR 37

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Search completed: Wed Jun 16 12:48:39 1999
Job time : 45 secs.

W P S R L F
***** (TM)

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Mpsrch_pp protein - protein database search, using Smith-Waterman algorithm

Run on: Wed Jun 16 12:51:39 1999; Maspar time 1.79 Seconds
Tabular output not generated. 209.779 Million cell updates/sec

Title: >VANDER-027-213.PEP
Description: (1-37) from vander027777.pep
Perfect Score: 279
Sequence: 1 LRALLTAPSLRRSSCFGGRMDRIGAGSLGCNSFRY 37

Scoring table: PAM 150
Gap 11

Searched: 106580 seqs, 10152877 residues

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database: a-issued
1:5A_COMB 2:5B_COMB 3:PCT9_COMB 4:backfiles1

Statistics: Mean 22.667; Variance 80.942; scale 0.280

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description	Pred. No.
1	279	100.0	136	4	5212286-4 Patent No. 5212286.	8.03e-22
2	279	100.0	151	4	5212286-2 Patent No. 5212286.	8.03e-22
3	264	94.6	152	4	5212286-6 Patent No. 5212286.	4.01e-20
4	252	90.3	144	4	5202239-1 Patent No. 5202239.	9.03e-19
5	252	90.3	144	4	5202239-3 Patent No. 5202239.	9.03e-19
6	242	86.7	32	4	5449751-3 Patent No. 5449751.	1.20e-17
7	242	86.7	32	4	5449751-1 Patent No. 5449751.	1.20e-17
8	242	86.7	32	1	US-08-451-1 Sequence 2, Applicatio	1.20e-17
9	242	86.7	32	2	US-08-451-1 Sequence 4, Applicatio	1.20e-17
10	242	86.7	32	3	PCT-US94-1 Sequence 2, Applicatio	1.20e-17
11	242	86.7	32	2	US-08-470-1 Sequence 18, Applicatio	1.20e-17
12	221	79.2	32	2	US-08-470-1 Sequence 5, Applicatio	2.67e-15
13	221	79.2	32	3	PCT-US94-1 Sequence 5, Applicatio	2.67e-15
14	221	79.2	32	1	US-08-451-1 Sequence 5, Applicatio	2.67e-15
15	216	77.4	28	4	5449751-2 Patent No. 5449751.	9.59e-15
16	216	77.4	28	4	5204327-1 Patent No. 5204327.	9.59e-15
17	216	77.4	28	1	US-08-297-1 Sequence 1, Applicatio	9.59e-15
18	216	77.4	28	1	US-07-828-1 Sequence 40, Applicatio	9.59e-15
19	216	77.4	28	1	US-07-754-1 Sequence 2, Applicatio	9.59e-15
20	216	77.4	28	1	US-08-184-1 Sequence 3, Applicatio	9.59e-15
21	216	77.4	28	1	US-07-828-1 Sequence 1, Applicatio	9.59e-15
22	216	77.4	28	1	US-08-066-1 Sequence 2, Applicatio	9.59e-15
23	216	77.4	28	2	US-08-470-1 Sequence 2, Applicatio	9.59e-15

ALIGNMENTS

RESULT 1	24	216	77.4	28	1	US-08-741-1	Sequence 2, Applicatio	9.59e-15
ID 5212286-4	25	216	77.4	28	4	5461142-1	Patent No. 5461142.	9.59e-15
XX	26	216	77.4	28	1	US-08-288-1	Sequence 2, Applicatio	9.59e-15
AC	27	216	77.4	28	3	PCT-US94-1	Sequence 21, Applicati	9.59e-15
XX	28	216	77.4	28	1	US-07-754-1	Sequence 2, Applicatio	9.59e-15
XX	29	216	77.4	28	1	US-08-451-0	Sequence 21, Applicati	9.59e-15
XX	30	216	77.4	28	3	PCT-US94-0	Sequence 1, Applicatio	9.59e-15
XX	31	216	77.4	29	2	US-08-448-1	Sequence 5, Applicatio	9.59e-15
XX	32	207	74.2	28	4	5204327-3	Patent No. 5204327.	9.53e-14
XX	33	207	74.2	28	2	US-08-470-1	Sequence 9, Applicatio	9.53e-14
XX	34	207	74.2	28	1	US-07-754-1	Sequence 3, Applicatio	9.53e-14
XX	35	207	74.2	28	1	US-08-451-1	Sequence 9, Applicatio	9.53e-14
XX	36	207	74.2	28	1	US-07-754-1	Sequence 3, Applicatio	9.53e-14
XX	37	207	74.2	28	2	US-08-457-1	Sequence 21, Applicati	9.53e-14
XX	38	207	74.2	28	1	US-08-240-1	Sequence 21, Applicati	9.53e-14
XX	39	207	74.2	28	3	PCT-US94-1	Sequence 9, Applicatio	9.53e-14
XX	40	205	73.5	28	1	US-07-781-1	Sequence 13, Applicati	1.59e-13
XX	41	205	73.5	28	1	US-07-781-1	Sequence 12, Applicati	1.59e-13
XX	42	205	73.5	28	1	US-07-781-1	Sequence 14, Applicati	1.59e-13
XX	43	204	73.1	28	1	US-07-778-1	Sequence 1, Applicatio	2.05e-13
XX	44	203	72.8	32	1	US-08-451-1	Sequence 15, Applicati	2.64e-13
XX	45	203	72.8	32	3	PCT-US94-1	Sequence 15, Applicati	2.64e-13

Query Match 100.0%; Score 279; DB 4; Length 136;
Best Local Similarity 100.0%; Pred. No. 8.03e-22;
Matches 37; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DB 100	LRALLTAPSLRRSSCFGGRMDRIGAGSLGCNSFRY 136
QY 1	LRALLTAPSLRRSSCFGGRMDRIGAGSLGCNSFRY 37
1	
1	LRALLTAPSLRRSSCFGGRMDRIGAGSLGCNSFRY 37

RESULT 2

ID 5212286-2	STANDARD;	PRT;	164 AA.
AC	xxxxxx		
XX			
XX			
DT 01-JAN-1900			
XX			
DE Patent No. 5212286.			
XX			
CC Patent No. 5212286			
CC APPLICANT: LEWICKI, JOHN A.; SCARBOROUGH, ROBERT M.			
CC TITLE OF INVENTION: ATRIAL NATRIURETIC/VASODILATOR			
CC PEPTIDE COMPOUNDS			
CC NUMBER OF SEQUENCES: 68			
CC CURRENT APPLICATION DATA:			
CC APPLICATION NUMBER: US/07/870,795			
CC FILING DATE: 05-JUN-1986			
CC PRIOR APPLICATION DATA:			
CC APPLICATION NUMBER: 766,030			
CC FILING DATE: 08-MAY-1985			
CC APPLICATION NUMBER: 602,117			
CC FILING DATE: 09-APR-1984			
CC APPLICATION NUMBER: 616,488			
CC FILING DATE: 01-JUN-1984			
CC SEQ ID NO:4:			
CC LENGTH: 136			
CC SEQUENCE 147 AA; 15978 MW; 112999 CN;			

CC APPLICANT: LEWICKI, JOHN A.:SCARBOROUGH, ROBERT M.
CC TITLE OF INVENTION: ATRIAL NATRIURETIC/VASODILATOR
CC PEPTIDE COMPOUNDS
CC NUMBER OF SEQUENCES: 68
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: US/07/870,795
CC FILING DATE: 05-JUN-1986
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: 766,030
CC FILING DATE: 08-MAY-1985
CC APPLICATION NUMBER: 602,117
CC FILING DATE: 09-APR-1984
CC APPLICATION NUMBER: 616,488
CC FILING DATE: 01-JUN-1984
CC SEQ ID NO:2:
CC LENGTH: 151
CC SEQUENCE 164 AA; 17827 MW; 143008 CN;
Query Match 100.0%; Score 279; DB 4; Length 151;
Best Local Similarity 100.0%; Pred. No. 8.03e-22;
Matches 37; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Db 115 LRLLTAPRSLRRSCFGGRMDRIGAGSLGCNSFRY 151
|||||
QY 1 LRLLTAPRSLRRSCFGGRMDRIGAGSLGCNSFRY 37
RESULT 3
ID 5212286-6 STANDARD; PRT; 165 AA.
XX AC xxxxxx
XX DE 01-JAN-1900
DT Patent No. 5212286.
DE Patent No. 5212286
XX Patent No. 5212286
CC APPLICANT: LEWICKI, JOHN A.:SCARBOROUGH, ROBERT M.
CC TITLE OF INVENTION: ATRIAL NATRIURETIC/VASODILATOR
CC PEPTIDE COMPOUNDS
CC NUMBER OF SEQUENCES: 68
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: US/07/870,795
CC FILING DATE: 05-JUN-1986
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: 766,030
CC FILING DATE: 08-MAY-1985
CC APPLICATION NUMBER: 602,117
CC FILING DATE: 09-APR-1984
CC APPLICATION NUMBER: 616,488
CC FILING DATE: 01-JUN-1984
CC SEQ ID NO:6:
CC LENGTH: 152
CC SEQUENCE 165 AA; 17987 MW; 141087 CN;
Query Match 94.6%; Score 264; DB 4; Length 152;
Best Local Similarity 91.9%; Pred. No. 4.01e-20;
Matches 34; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
Db 114 LRLLAGPRSLRRSCFGGRIDRIGAGSLGCNSFRY 150
|||||
QY 1 LRLLTAPRSLRRSCFGGRMDRIGAGSLGCNSFRY 37
RESULT 4
ID 5202239-1 STANDARD; PRT; 156 AA.
XX AC xxxxxx
XX DE 01-JAN-1900
DT Patent No. 5202239.
DE Patent No. 5202239.

CC Patent No. 5202239
CC APPLICANT: TARNOWSKI, JOSEPH S.:HILLIKER, SANDRA; WILLETT,
CC SCOTT W.
CC TITLE OF INVENTION: EXPRESSION OF RECOMBINANT POLYPEPTIDES
CC WITH IMPROVED PURIFICATION
CC NUMBER OF SEQUENCES: 16
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: US/08/564,259
CC FILING DATE: 07-AUG-1990
CC SEQ ID NO:1:
CC LENGTH: 144
CC SEQUENCE 156 AA; 17116 MW; 129679 CN;
Query Match 90.3%; Score 252; DB 4; Length 144;
Best Local Similarity 92.3%; Pred. No. 9.03e-19;
Matches 36; Conservative 1; Mismatches 0; Indels 2; Gaps 1;
Db 106 LRLLTAPRSLKFRSCFGGRMDRIGAGSLGCNSFRY 144
|||||
QY 1 LRLLTAPRSLR--RSCFGGRMDRIGAGSLGCNSFRY 37
RESULT 5
ID 5202239-3 STANDARD; PRT; 156 AA.
XX AC xxxxxx
XX DT 01-JAN-1900
DT Patent No. 5202239.
DE Patent No. 5202239
XX Patent No. 5202239
CC APPLICANT: TARNOWSKI, JOSEPH S.:HILLIKER, SANDRA; WILLETT,
CC SCOTT W.
CC TITLE OF INVENTION: EXPRESSION OF RECOMBINANT POLYPEPTIDES
CC WITH IMPROVED PURIFICATION
CC NUMBER OF SEQUENCES: 16
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: US/08/564,259
CC FILING DATE: 07-AUG-1990
CC SEQ ID NO:3:
CC LENGTH: 144
CC SEQUENCE 156 AA; 17115 MW; 129665 CN;
Query Match 90.3%; Score 252; DB 4; Length 144;
Best Local Similarity 92.3%; Pred. No. 9.03e-19;
Matches 36; Conservative 1; Mismatches 0; Indels 2; Gaps 1;
Db 106 LRLLTAPRSLKFRSCFGGRMDRIGAGSLGCNSFRY 144
|||||
QY 1 LRLLTAPRSLR--RSCFGGRMDRIGAGSLGCNSFRY 37
RESULT 6
ID 5449751-3 STANDARD; PRT; 35 AA.
XX AC xxxxxx
XX DT 01-JAN-1900
DT Patent No. 5449751.
DE Patent No. 5449751
XX Patent No. 5449751
CC APPLICANT: FORSSMANN, WOLF-GEORG; ALT, JEANETTE M.; BECKER,
CC GERHARD; HERBST, FRANZ
CC TITLE OF INVENTION: CARDIODILATIN FRAGMENT, PROCESS FOR
CC PREPARING SAME AND USE THEREOF
CC NUMBER OF SEQUENCES: 4
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: US/08/185,240
CC FILING DATE: 24-JAN-1994
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: 994,084

CC FILING DATE: 16-DEC-1992
CC APPLICATION NUMBER: 795,248
CC FILING DATE: 18-NOV-1991
CC APPLICATION NUMBER: 401,401
CC FILING DATE: 01-SEP-1989
CC APPLICATION NUMBER: 100,144
CC FILING DATE: 28-AUG-1987
CC SEQ ID NO: 3
CC LENGTH: 32
CC SEQUENCE 35 AA; 3838 MW; 6483 CN;

Query Match 86.7%; Score 242; DB 4; Length 32;
Best Local Similarity 100.0%; Pred. No. 1.20e-17;
Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 1 TAPSLRRSCFGGRMDRIGAGSLGNCNFRY 32
|||||
Qy 6 TAPSLRRSCFGGRMDRIGAGSLGNCNFRY 37
|||||

RESULT 7
ID 5449751-1 STANDARD; PRT; 35 AA.

XX AC xxxxxx
XX 01-JAN-1900
XX Patent No. 5449751.

XX Patent No. 5449751
CC APPLICANT: FORSMANN, WOLF-GEORG; ALT, JEANNETTE M.; BECKER,
CC GERHARD; HERBST, FRANZ
CC TITLE OF INVENTION: CARDIODILATIN FRAGMENT, PROCESS FOR
CC PREPARING SAME AND USE THEREOF
CC NUMBER OF SEQUENCES: 4

CC CURRENT APPLICATION DATA:
CC FILING DATE: 24-JAN-1994
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: 994,084
CC FILING DATE: 16-DEC-1992
CC APPLICATION NUMBER: 795,248
CC FILING DATE: 18-NOV-1991
CC APPLICATION NUMBER: 401,401
CC FILING DATE: 01-SEP-1989
CC APPLICATION NUMBER: 100,144
CC FILING DATE: 28-AUG-1987
CC SEQ ID NO: 1
CC LENGTH: 32
CC SEQUENCE 35 AA; 3838 MW; 6483 CN;

Query Match 86.7%; Score 242; DB 4; Length 32;
Best Local Similarity 100.0%; Pred. No. 1.20e-17;
Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 1 TAPSLRRSCFGGRMDRIGAGSLGNCNFRY 32
|||||
Qy 6 TAPSLRRSCFGGRMDRIGAGSLGNCNFRY 37
|||||

RESULT 8
ID US-08-451-240-2 STANDARD; PRT; 32 AA.

XX AC xxxxxx
XX DT
XX DT
XX DT
XX Sequence 2, Application US/08451240
XX Sequence 2, Application US/08451240
CC Patent No. 5665704
CC GENERAL INFORMATION:
CC APPLICANT: Lowe, David

CC APPLICANT: Cunningham, Brian
CC APPLICANT: Oare, David
CC APPLICANT: McDowell, Robert S.
CC APPLICANT: Burnier, John
CC TITLE OF INVENTION: RECEPTOR SPECIFIC ATRIAL NATRIURETIC
CC TITLE OF INVENTION: PEPTIDES
CC NUMBER OF SEQUENCES: 47
CC CORRESPONDENCE ADDRESS:
CC ADDRESSEE: Genentech, Inc.
CC STREET: 460 Point San Bruno Blvd
CC CITY: South San Francisco
CC STATE: California
CC COUNTRY: USA
CC ZIP: 94080

CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: 5.25 inch, 360 kb floppy disk
CC COMPUTER: IBM PC compatible
CC OPERATING SYSTEM: PC-DOS/MS-DOS
CC SOFTWARE: patin (Genentech)
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: US/08/451,240
CC FILING DATE:
CC CLASSIFICATION: 530

CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: 08/362552
CC FILING DATE: 06-JAN-1995
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: 08/152994
CC FILING DATE: 12-NOV-1993
CC ATTORNEY/AGENT INFORMATION:
CC NAME: Kubinec, Jeffrey S.
CC REGISTRATION NUMBER: 36,575
CC REFERENCE/DOCKET NUMBER: P0844PIC1
CC TELECOMMUNICATION INFORMATION:
CC TELEPHONE: 415/225-8228
CC TELEFAX: 415/952-9881
CC TELEFAX: 910/371-7168
CC INFORMATION FOR SEQ ID NO: 2:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 32 amino acids
CC TYPE: amino acid
CC TOPOLOGY: linear
CC SEQUENCE 32 AA; 3508 MW; 4652 CN;

Query Match 86.7%; Score 242; DB 1; Length 32;
Best Local Similarity 100.0%; Pred. No. 1.20e-17;
Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 1 TAPSLRRSCFGGRMDRIGAGSLGNCNFRY 32
|||||
Qy 6 TAPSLRRSCFGGRMDRIGAGSLGNCNFRY 37
|||||

RESULT 9
ID US-08-737-927-4 STANDARD; PRT; 32 AA.

XX AC xxxxxx
XX DT
XX DT
XX DT
XX Sequence 4, Application US/08737927
XX Sequence 4, Application US/08737927
CC Patent No. 5767239
CC GENERAL INFORMATION:
CC APPLICANT: IMMER, Hansueli
CC APPLICANT: FORSMANN, Wolf-Georg
CC APPLICANT: ADERMAN, Knut
CC APPLICANT: KLESSEN, Christian
CC TITLE OF INVENTION: PREPARING CARDIODILATIN FRAGMENTS, AND HIGHLY PURIF.
CC TITLE OF INVENTION: CARDIODILATIN FRAGMENTS
CC NUMBER OF SEQUENCES: 5

```

AC      xxxxxx
XX
XX
DT
DT
XX
XX
DE
XX
Sequence 2, Application PC/TUS9412591
Sequence 2, Application PC/TUS9412591
CC
CC  GENERAL INFORMATION:
CC  APPLICANT: Genentech, Inc.
CC  APPLICANT: Lowe, David
CC  APPLICANT: Cunningham, Brian C.
CC  APPLICANT: Oare, David
CC  APPLICANT: McDowell, Robert S.
CC  APPLICANT: Burnier, John
CC  TITLE OF INVENTION: RECEPTOR SPECIFIC ATRIAL NATRIURETIC
CC  TITLE OF INVENTION: PEPTIDES
CC  NUMBER OF SEQUENCES: 47
CC  CORRESPONDENCE ADDRESS:
CC  ADDRESSEE: Genentech, Inc.
CC  STREET: 460 Point San Bruno Blvd
CC  CITY: South San Francisco
CC  STATE: California
CC  COUNTRY: USA
CC  ZIP: 94080
CC  COMPUTER READABLE FORM:
CC  MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk

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CC	COMPUTER:	IBM PC compatible
CC	OPERATING SYSTEM:	PC-DOS/MS-DOS
CC	SOFTWARE:	patin (Genentech)
CC	CURRENT APPLICATION DATA:	
CC	APPLICATION NUMBER:	PCT/US94/12591
CC	FILING DATE:	
CC	CLASSIFICATION:	
CC	PRIOR APPLICATION DATA:	
CC	APPLICATION NUMBER:	08/152994
CC	FILING DATE:	12-NOV-1993
CC	ATTORNEY/AGENT INFORMATION:	
CC	NAME:	Winter, Daryl B.
CC	REGISTRATION NUMBER:	32,637
CC	REFERENCE/DOCKET NUMBER:	844P1
CC	TELECOMMUNICATION INFORMATION:	
CC	TELEPHONE:	415/325-1249
CC	TELEFAX:	415/952-9881
CC	TELEX:	910/371-7168
CC	INFORMATION FOR SEQ ID NO: 2:	
CC	SEQUENCE CHARACTERISTICS:	
CC	LENGTH:	32 amino acids
CC	TYPE:	amino acid
CC	TOPOLOGY:	linear
CC	SEQUENCE	32 AA; 3508 MW; 4652 CN;
SQ	Query Match	86.7%; Score 242; D
	Best Local Similarity	100.0%; Pred. No. 1.2
	Matches	32; Conservative 0; Mismatch
Db	1 TAPRSRRSCFGGRMDRIGAQSLGCGNSFRY 32	
QY	6 TAPRSRRSCFGGRMDRIGAQSLGCGNSFRY 37	
RESULT	11	
ID	US-08-470-846A-18	STANDARD: PRT:
XX	AC AC	
XX	xxxxxx	
DT		
DT		
DE	Sequence 18; Application US/08470846A	
XX		
CC	Sequence 18, Application US/08470846A	
CC	Patent No. 5846932	
CC	GENERAL INFORMATION:	
CC	APPLICANT: Genentech, Inc.	
CC	APPLICANT: Lowe, David G.	
CC	APPLICANT: Cunningham, Brian C.	
CC	APPLICANT: Oare, David	
CC	APPLICANT: McDowell, Robert S.	
CC	APPLICANT: Burnier, John	
CC	TITLE OF INVENTION: RECEPTOR SPECIFICITY	
CC	NUMBER OF SEQUENCES: 43	
CC	CORRESPONDENCE ADDRESS:	
CC	ADDRESSEE: Genentech, Inc.	
CC	STREET: 460 Point San Bruno Blvd	
CC	CITY: South San Francisco	
CC	STATE: California	
CC	COUNTRY: USA	
CC	ZIP: 94080	
CC	COMPUTER READABLE FORM:	
CC	MEDIUM TYPE: 3.5 inch, 1.44 Mb flo	
CC	COMPUTER: IBM PC compatible	
CC	OPERATING SYSTEM: PC-DOS/MS-DOS	
CC	SOFTWARE: winpatin (genentech)	
CC	CURRENT APPLICATION DATA:	
CC	APPLICATION NUMBER:	US/08/470,846A
CC	FILING DATE:	06-Jun-1995
CC	CLASSIFICATION:	514
CC	PRIOR APPLICATION DATA:	
CC	APPLICATION NUMBER:	08/419877
CC	FILING DATE:	11-APR-1995

CC PRIOR APPLICATION DATA: 08/362552
CC APPLICATION NUMBER: 08/362552
CC FILING DATE: 06-JAN-1995
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: 08/152994
CC FILING DATE: 12-NOV-1993
CC ATTORNEY/AGENT INFORMATION:
CC NAME: Kubinec, Jeffrey S.
CC REGISTRATION NUMBER: 36,575
CC REFERENCE/DOCKET NUMBER: P0844P2C1
CC TELEPHONE: 415/225-8228
CC TELEFAX: 415/952-9881
CC TELEX: 910/371-7168
CC INFORMATION FOR SEQ ID NO: 18:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 32 amino acids
CC TYPE: Amino Acid
CC TOPOLOGY: Linear
CC SEQUENCE 32 AA; 3508 MW; 4652 CN;

Query Match 86.7%; Score 242; DB 2; Length 32;
Best Local Similarity 100.0%; Pred. No. 1.20e-17;
Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 1 TAPSLRRSCFGGRMDRIGAQSGGLGCNSFRY 32
|||||
Qy 6 TAPSLRRSCFGGRMDRIGAQSGGLGCNSFRY 37

RESULT 12
ID US-08-470-846A-5 STANDARD; PRT; 32 AA.

XX AC xxxxxx
XX DT
XX DE
XX Sequence 5, Application US/08470846A
XX Sequence 5, Application US/08470846A
XX Patent No. 5846932
XX GENERAL INFORMATION:
XX APPLICANT: Genentech, Inc.
XX APPLICANT: Lowe, David G.
XX APPLICANT: Cunningham, Brian C.
XX APPLICANT: Oare, David
XX APPLICANT: McDowell, Robert S.
XX APPLICANT: Burnier, John
XX TITLE OF INVENTION: RECEPTOR SPECIFIC ATRIAL NATRIURETIC PEPTIDES
XX NUMBER OF SEQUENCES: 43
XX CORRESPONDENCE ADDRESS:
XX ADDRESSEE: Genentech, Inc.
XX STREET: 460 Point San Bruno Blvd
XX CITY: South San Francisco
XX STATE: California
XX COUNTRY: USA
XX ZIP: 94080
XX COMPUTER READABLE FORM:
XX MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
XX COMPUTER: IBM PC compatible
XX OPERATING SYSTEM: PC-DOS/MS-DOS
XX SOFTWARE: WinPatIn (Genentech)
XX CURRENT APPLICATION DATA:
XX APPLICATION NUMBER: US/08/470,846A
XX FILING DATE: 06-Jun-1995
XX CLASSIFICATION: 514
XX PRIOR APPLICATION DATA:
XX APPLICATION NUMBER: 08/419877
XX FILING DATE: 11-APR-1995
XX PRIOR APPLICATION DATA:
XX APPLICATION NUMBER: 08/362552
XX FILING DATE: 06-JAN-1995
XX PRIOR APPLICATION DATA:

CC APPLICATION NUMBER: 08/152994
CC FILING DATE: 12-NOV-1993
CC ATTORNEY/AGENT INFORMATION:
CC NAME: Kubinec, Jeffrey S.
CC REGISTRATION NUMBER: 36,575
CC REFERENCE/DOCKET NUMBER: P0844P2C1
CC TELEPHONE: 415/225-8228
CC TELEFAX: 415/952-9881
CC TELEX: 910/371-7168
CC INFORMATION FOR SEQ ID NO: 5:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 32 amino acids
CC TYPE: Amino Acid
CC TOPOLOGY: Linear
CC SEQUENCE 32 AA; 3589 MW; 4484 CN;

Query Match 79.2%; Score 221; DB 2; Length 32;
Best Local Similarity 93.8%; Pred. No. 2.67e-15;
Matches 30; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Db 1 TAPSLRRSCFGGRMDRIGAQSGGLGCNSFRY 32
|||||
Qy 6 TAPSLRRSCFGGRMDRIGAQSGGLGCNSFRY 37

RESULT 13
ID PCT-US94-12591-5 STANDARD; PRT; 32 AA.

XX AC xxxxxx
XX DT
XX DE
XX Sequence 5, Application PC/TUS9412591
XX Sequence 5, Application PC/TUS9412591
XX GENERAL INFORMATION:
XX APPLICANT: Genentech, Inc.
XX APPLICANT: Lowe, David
XX APPLICANT: Cunningham, Brian C.
XX APPLICANT: Oare, David
XX APPLICANT: McDowell, Robert S.
XX APPLICANT: Burnier, John
XX TITLE OF INVENTION: RECEPTOR SPECIFIC ATRIAL NATRIURETIC
XX NUMBER OF SEQUENCES: 47
XX CORRESPONDENCE ADDRESS:
XX ADDRESSEE: Genentech, Inc.
XX STREET: 460 Point San Bruno Blvd
XX CITY: South San Francisco
XX STATE: California
XX COUNTRY: USA
XX ZIP: 94080
XX COMPUTER READABLE FORM:
XX MEDIUM TYPE: 5.25 inch, 360 kb floppy disk
XX COMPUTER: IBM PC compatible
XX OPERATING SYSTEM: PC-DOS/MS-DOS
XX SOFTWARE: patin (Genentech)
XX CURRENT APPLICATION DATA:
XX APPLICATION NUMBER: PCT/US94/12591
XX FILING DATE:
XX CLASSIFICATION:
XX PRIOR APPLICATION DATA:
XX APPLICATION NUMBER: 08/152994
XX FILING DATE: 12-NOV-1993
XX ATTORNEY/AGENT INFORMATION:
XX NAME: Winter, Daryl B.
XX REGISTRATION NUMBER: 32,637
XX REFERENCE/DOCKET NUMBER: 844P1
XX TELECOMMUNICATION INFORMATION:
XX TELEPHONE: 415/225-1249
XX TELEFAX: 415/952-9881
XX TELEX: 910/371-7168

CC INFORMATION FOR SEQ ID NO: 5:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 32 amino acids
CC TYPE: amino acid
CC TOPOLOGY: linear
SQ SEQUENCE 32 AA; 3589 MW; 4484 CN;

Query Match 79.2%; Score 221; DB 3; Length 32;
Best Local Similarity 93.8%; Pred. No. 2.67e-15;
Matches 30; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Db 1 TAPSLRRSCFGGRIDRIRAOGLGCSNFRY 32
|||||
Qy 6 TAPSLRRSCFGGRMDRIGAOGLGCSNFRY 37

RESULT 14
ID US-08-451-240-5 STANDARD; PRT; 32 AA.
XX AC
XX XXXXXX
XX

Sequence 5, Application US/08451240
Patent No. 5665704

GENERAL INFORMATION:
APPLICANT: Lowe, David
APPLICANT: Cunningham, Brian
APPLICANT: Oate, David
APPLICANT: McDowell, Robert S.
APPLICANT: Burnier, John
TITLE OF INVENTION: RECEPTOR SPECIFIC ATRIAL NATRIURETIC
TITLE OF INVENTION: PEPTIDES
NUMBER OF SEQUENCES: 47
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Genentech, Inc.
STREET: 450 Point San Bruno Blvd
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080

COMPUTER READABLE FORM:
MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: patin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/451,240
FILING DATE:

CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/362552
FILING DATE: 06-JAN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/152994
FILING DATE: 12-NOV-1993
ATTORNEY/AGENT INFORMATION:
NAME: Kubinec, Jeffrey S.
REGISTRATION NUMBER: 36,575
REFERENCE/DOCKET NUMBER: P0844P1C1
TELEPHONE: 415/225-8228
TELEFAX: 415/952-9881
TELEX: 910/371-7168

INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 32 amino acids
TYPE: amino acid
TOPOLOGY: linear
SEQUENCE 32 AA; 3589 MW; 4484 CN;

Query Match 79.2%; Score 221; DB 1; Length 32;
Best Local Similarity 93.8%; Pred. No. 2.67e-15;
Matches 30; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Db 1 TAPSLRRSCFGGRIDRIRAOGLGCSNFRY 32
|||||
Qy 6 TAPSLRRSCFGGRMDRIGAOGLGCSNFRY 37

RESULT 15
ID 5449751-2 STANDARD; PRT; 30 AA.

XX AC
XX XXXXXX
XX 01-JAN-1900
XX Patent No. 5449751.

Patent No. 5449751
APPLICANT: FORSSMANN, WOLF-GEORG; ALT, JEANETTE M.; BECKER, GERHARD; HERBST, FRANZ

TITLE OF INVENTION: CARDIODILATIN FRAGMENT, PROCESS FOR PREPARING SAME AND USE THEREOF
NUMBER OF SEQUENCES: 4

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/185,240
FILING DATE: 24-JAN-1994

PRIOR APPLICATION DATA:
APPLICATION NUMBER: 994,084

FILING DATE: 16-DEC-1992

APPLICATION NUMBER: 795,248

FILING DATE: 18-NOV-1991

APPLICATION NUMBER: 401,401

FILING DATE: 01-SEP-1989

APPLICATION NUMBER: 100,144

FILING DATE: 28-AUG-1987

SEQ ID NO: 2

LENGTH: 28

SEQUENCE 30 AA; 3303 MW; 4581 CN;

Query Match 77.4%; Score 216; DB 4; Length 28;
Best Local Similarity 100.0%; Pred. No. 9.59e-15;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 1 SLRRSCFGGRMDRIGAOGLGCSNFRY 28
|||||
Qy 10 SLRRSCFGGRMDRIGAOGLGCSNFRY 37

Search completed: Wed Jun 16 12:51:46 1999
Job time : 7 secs.

W P S R E L

(TM)

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Distribution rights by Oxford Molecular Ltd

MPSrch_pp protein - protein database search, using Smith-Waterman algorithm

Run on: Wed Jun 16 12:48:57 1999; Maspar time 4.75 Seconds
Tabular output not generated. 311.884 Million cell updates/sec

Title: >VANDER-027-213.PEP
Description: (1-37) from vander027777.p
Perfect Score: 279
Sequence: 1 LRALLTAPSLRRSCFGGMDRIGNQSLGNCSPRY 37

Scoring table: PAM 150
Gap 11
Searched: 122810 seqs, 40068593 residues

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database: pir60
1:pir1 2:pir2 3:pir3 4:pir4

Statistics: Mean 32.756; Variance 52.653; scale 0.622

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description	Pred. No.
1	279	100.0	151	1 AWBU	natriuretic peptide A	3.82e-45
2	279	100.0	152	1 AWBO	atrial natriuretic pe	3.82e-45
3	276	98.9	149	1 AWBG	atrial natriuretic pe	2.01e-44
4	276	98.9	150	1 SL13107	atrial natriuretic pe	2.01e-44
5	276	98.9	153	2 SL14873	atrial natriuretic pe	2.01e-44
6	270	96.8	153	1 AWBR	atrial natriuretic pe	5.99e-43
7	267	95.7	128	2 SL14872	atrial natriuretic pe	2.86e-42
8	264	94.6	152	1 AWRT	atrial natriuretic fa	1.49e-41
9	264	94.6	152	1 AWMS	atrial natriuretic pe	1.49e-41
10	220	78.9	161	4 I55480	hypothetical natriure	3.45e-31
11	199	71.3	145	2 J00947	atrial natriuretic pe	2.37e-26
12	172	61.6	30	2 S01657	atrial natriuretic fa	2.85e-20
13	160	57.3	103	2 A14403	aldosterone secretion	1.25e-17
14	157	56.3	131	2 A33873	brain natriuretic pep	5.61e-17
15	157	56.3	131	2 A31676	brain natriuretic fac	5.61e-17
16	155	55.6	105	2 B36736	brain natriuretic pep	1.52e-16
17	143	51.3	140	2 SL14320	alpha-atrial natriure	5.70e-14
18	131	47.0	36	2 SL5621	ventricular natriuret	1.87e-11
19	129	46.2	134	1 AWHUB	natriuretic peptide B	4.83e-11
20	125	44.8	27	2 JC1081	brain natriuretic pep	3.19e-10
21	124	44.4	27	2 A33431	atrial natriuretic fa	5.10e-10
22	118	42.3	121	2 A30162	brain natriuretic fac	8.29e-09
23	117	41.9	37	2 S71382	lebetin 2 isoform bet	1.31e-08

24	117	41.9	38	2 S71381	lebetin 2 isoform alp	1.31e-08
25	114	40.9	22	2 JT0581	natriuretic peptide t	5.18e-08
26	107	38.4	115	2 SL5822	natriuretic peptide t	1.21e-06
27	107	38.4	126	2 A36155	natriuretic peptide c	1.21e-06
28	107	38.4	126	2 A55688	brain natriuretic pep	1.21e-06
29	107	38.4	126	2 SL2988	natriuretic peptide c	1.21e-06
30	107	38.4	126	1 AWHUC	natriuretic peptide t	1.21e-06
31	107	38.4	135	2 A61244	natriuretic peptide t	1.21e-06
32	106	38.0	121	2 A49144	type-B natriuretic pe	1.88e-06
33	106	38.0	121	2 I49548	brain natriuretic pep	1.88e-06
34	104	37.3	118	2 B54119	C-type natriuretic pe	4.56e-06
35	102	36.6	22	2 A36399	C-type natriuretic pe	1.09e-05
36	102	36.6	129	2 A54119	C-type natriuretic pe	1.09e-05
37	101	36.2	22	2 A35418	brain natriuretic pep	1.69e-05
38	92	33.0	22	2 A42974	natriuretic peptide,	7.80e-04
39	85	30.5	298	2 T01548	hypothetical protein	1.36e-02
40	80	28.7	187	2 B69314	hypothetical protein	9.78e-02
41	78	28.0	334	2 H69214	glucosamine--fructose	2.11e-01
42	78	28.0	763	2 S23457	polysulfide reductase	2.11e-01
43	74	26.5	639	2 A48900	tetracycline resistanc	9.46e-01
44	74	26.5	691	2 S44280	receptor tyrosine kin	9.46e-01
45	74	26.5	984	2 A34076	protein-tyrosine kin	9.46e-01

ALIGNMENTS

RESULT	ENTRY	AWBU	#type complete
1	natriuretic peptide A precursor - human		
ENTRY	ANF: atrial natriuretic factor; atrial natriuretic protein;		
TITLE	prepronatriodilatin (PND)		
ALTERNATE_NAMES	atrial alpha natriuretic peptide (ANP); cardioidilatin (atrial		
CONTAINS	gamma natriuretic factor)		
ORGANISM	#formal_name Homo sapiens #common_name man		
DATE	15-Nov-1984 #sequence_revision 15-Nov-1984 #text_change		
ACCESSIONS	20-Mar-1998		
REFERENCE	A22693; B22693; A01424; B29370; A32733; I58054; S14097;		
#authors	I39458; I39459; I37167		
#journal	Nemer, M.; Chamberland, M.; Sirolis, D.; Argentin, S.; Drouin,		
#title	J.; Dixon, R.A.F.; Zivin, R.A.; Condra, J.H.		
#cross-references	Nature (1984) 312:654-656		
#accession	Gene structure of human cardiac hormone precursor,		
#molecule_type	preonatriodilatin.		
#residues	#molecule_type DNA		
#cross-references	1-151 #label NEM		
#accession	#cross-references GB:X01470; NID:g28687; PID:g825625		
#molecule_type	1-151 #label NE2		
#residues	allelic variant with UGA termination codon replaced by		
#note	CGA arginine codon		
REFERENCE	A01424		
#authors	Oikawa, S.; Imai, M.; Ueno, A.; Tanaka, S.; Noguchi, T.;		
#journal	Nakazato, H.; Kangawa, K.; Fukuda, A.; Matsuo, H.		
#title	Nature (1984) 309:724-726		
#cross-references	Cloning and sequence analysis of cDNA encoding a precursor		
#accession	for human atrial natriuretic polypeptide.		
#molecule_type	mRNA		
#residues	A01424		
#cross-references	#cross-references GB:K02043; NID:g178629; PID:g178630		
#accession	A29370		
REFERENCE	Seidman, C.E.; Bloch, K.D.; Klein, K.A.; Smith, J.A.;		
#authors	Science (1984) 226:1206-1209		
#journal	Nucleotide sequences of the human and mouse atrial		
#title	natriuretic factor genes.		
#cross-references	#cross-references MUID:85065766		
#accession	B29370		

```

##molecule_type DNA
##residues 1-64,'D',66-151 ##label SEI
##cross-references GB:K02043
REFERENCE
A32733
#authors Kangawa, K.; Matsuo, H.
#journal Biochem. Biophys. Res. Commun. (1984) 118:131-139
#title Purification and complete amino acid sequence of alpha-human
        atrial natriuretic polypeptide (alpha-hANP).
#cross-references MUID:841128019
#accession A32733
##molecule_type protein
##residues 124-151 ##label KAN
REFERENCE
I58054
#authors Nakayama, K.; Ohkubo, H.; Hirose, T.; Inayama, S.; Nakanishi,
        S.
#journal Nature (1984) 310:699-701
#title mRNA sequence for human cardiodilatin-atrial natriuretic
        factor precursor and regulation of precursor mRNA in rat
        atria.
#cross-references MUID:84295577
#accession I58054
##status translated from GB/EMBL/DBJ
##molecule_type mRNA
##residues 1-151 ##label RES
##cross-references GB:M30262; NID:g180181; PID:g180182
REFERENCE
S14097
#authors Vanneste, Y.; Michel, A.; Deschodt-Lanckman, M.
#journal Eur. J. Biochem. (1991) 196:281-286
#title Hydrolysis of intact and Cys-Phe-cleaved human atrial
        natriuretic peptide in vitro by human tissue kallikrein.
#cross-references MUID:91176998
#accession S14097
##molecule_type protein
##residues 124-151 ##label VAN
##note natural and synthetic peptide subjected to kallikrein
        proteolysis
REFERENCE
I39458
#authors Zivin, R.A.; Condra, J.H.; Dixon, R.A.; Seidah, N.G.;
        Chretien, M.; Nemer, M.; Chamberland, M.; Drouin, J.
#journal Proc. Natl. Acad. Sci. U.S.A. (1984) 81:6325-6329
#title Molecular cloning and characterization of DNA sequences
        encoding rat and human atrial natriuretic factors.
#cross-references MUID:85038509
#accession I39458
##status preliminary; translated from GB/EMBL/DBJ
##molecule_type mRNA
##residues 119-151,'RR' ##label RE2
##cross-references GB:K02044; NID:g178631; PID:g178632
REFERENCE
I39459
#authors Maki, M.; Parmentier, M.; Inagami, T.
#journal Biochem. Biophys. Res. Commun. (1984) 125:797-802
#title Cloning of genomic DNA for human atrial natriuretic factor.
#cross-references MUID:85096983
#accession I39459
##status preliminary; translated from GB/EMBL/DBJ
##molecule_type DNA
##residues 1-75 ##label RE3
##cross-references GB:K02399; NID:g178633; PID:g178634
REFERENCE
I39460
#authors Seidman, C.E.; Bloch, K.D.; Zisfein, J.; Smit, J.; Haber, E.;
        Homcy, C.J.; Duby, A.D.; Choi, E.; Graham, R.M.; Seidman,
        J.G.
#journal Hypertension (1985) 7:31-34
#title Molecular studies of the atrial natriuretic factor gene.
#accession I39460
##status translated from GB/EMBL/DBJ
##molecule_type DNA
##residues 1-64,'D',66-151 ##label RE4
##cross-references GB:IM54951; NID:g178636; PID:g178638
REFERENCE
I37167
#authors Greenberg, B.D.; Bencen, G.H.; Seilhamer, J.J.; Lewicki,
        J.A.; Fiddes, J.C.
#journal Nature (1984) 312:656-658

```

```

#title Nucleotide sequence of the gene encoding human atrial
        natriuretic factor precursor.
#cross-references MUID:85061627
#accession I37167
##status translated from GB/EMBL/DBJ
##molecule_type DNA
##residues 26-151 ##label RE5
##cross-references EMBL:X01471; NID:g28690
COMMENT Cardiodilatin is a vasoconstrictor but not a diuretic or
        natriuretic.
GENETICS
#gene GDB:NPPA; ANP; PND
##cross-references GDB:118727; OMIM:108780
#map_position lp36-lp36
#introns 41/3; 150/3
KEYWORDS
FEATURE
1-25 #domain signal sequence #status predicted #label SIG\
26-151 #product cardiodilatin #status predicted #label CDD\
124-151 #product atrial alpha natriuretic peptide #status
        predicted #label ANP\
130-146 #disulfide_bonds #status experimental
SUMMARY
#length 151 #molecular-weight 16395 #checksum 3644
Query Match 100.0%; Score 279; DB 1; Length 151;
Best Local Similarity 100.0%; Pred. No. 3,82e-45;
Matches 37; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Db 115 LRALLTAPSLRRSSCFGGMRDRIGAQSGLGCNSFRY 151
QY 1 LRALLTAPSLRRSSCFGGMRDRIGAQSGLGCNSFRY 37
|||||
RESULT 2
ENTRY #type complete
TITLE atrial natriuretic peptide precursor - bovine
ALTERNATE_NAMES ANP; atrial natriuretic polypeptide
ORGANISM #formal_name Bos primigenius taurus #common_name cattle
DATE 30-Jun-1989 #sequence_revision 30-Jun-1989 #text_change
20-Mar-1998
ACCESSIONS A90124; A93049; A24247; A26090
REFERENCE A90124
#authors Vlasuk, G.P.; Miller, J.; Bencen, G.H.; Lewicki, J.A.
#journal Biochem. Biophys. Res. Commun. (1986) 136:396-403
#title Structure and analysis of the bovine atrial natriuretic
        peptide precursor gene.
#cross-references MUID:86215205
#accession A90124
##molecule_type DNA
##residues 1-152 ##label VLA
##cross-references GB:M13145; NID:g162665; PID:g162666
REFERENCE A93049
#authors Ong, H.; McNicoll, N.; Lazure, C.; Seidah, N.; Chretien, M.;
        Cantin, M.; De Lean, A.
#journal Life Sci. (1986) 38:1309-1315
#title Purification and sequence determination of bovine atrial
        natriuretic factor.
#cross-references MUID:86173941
#accession A93049
##molecule_type protein
##residues 123-150 ##label ONG
GENETICS
#introns 40/3; 149/3
KEYWORDS #superfamily natriuretic peptide A precursor
FEATURE atrium; diuretic; hormone; natriuretic; osmoregulation
1-24 #domain signal sequence #status predicted #label SIG\
25-152 #product gamma atrial natriuretic factor #status
        predicted #label ANP\
123-150 #product alpha atrial natriuretic peptide #status
        experimental #label ANP\
129-145 #disulfide_bonds #status predicted

```



```
##molecule_type mRNA
##residues 1-153 ##label OIK
##cross-references GB:M12046; NID:g164770; PID:g164771
CLASSIFICATION #superfamily natriuretic peptide A precursor
KEYWORDS atrium; diuretic; hormone; natriuretic; osmoregulation
FEATURE
1-25 #domain signal sequence #status predicted #label SIG\
26-151 #product gamma atrial natriuretic factor #status
predicted #label ANF\
124-151 #product alpha atrial natriuretic peptide #status
predicted #label ANP\
130-146 #disulfide_bonds #status predicted
SUMMARY #length 153 #molecular_weight 16843 #checksum 7650

Query Match 96.8%; Score 270; DB 1; Length 153;
Best Local Similarity 97.3%; Pred. No. 5.49e-43;
Matches 36; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Db 115 LRALLTAPSLRRSSCGFRIDRIGAQSLGCSNFRY 151
Qy 1 LRALLTAPSLRRSSCGFRIDRIGAQSLGCSNFRY 37

RESULT 7
ENTRY #type fragment
TITLE atrial natriuretic peptide precursor - guinea pig (fragment)
ORGANISM #formal_name Cavia porcellus #common_name guinea pig
DATE 20-Feb-1995 #sequence_revision 30-Jan-1998 #text_change
20-Mar-1998
ACCESSIONS S14872
REFERENCE S14872
#authors Maegert, H.J.; Hanke, M.; Schmedding, G.; Teuteberg, K.;
Schulz-Knappe, P.; Forssmann, W.G.
#submission submitted to the EMBL Data Library, March 1991
#accession S14872
##molecule_type mRNA
##residues 1-128 ##label MAE
##cross-references EMBL:X58562; NID:g49543; PID:g49544
#experimental_source heart atria; adult
CLASSIFICATION #superfamily natriuretic peptide A precursor
KEYWORDS atrium; diuretic; hormone; natriuretic; osmoregulation
FEATURE
1-98 #domain signal sequence #status predicted #label SIG\
99-128 #product alpha atrial natriuretic peptide #status predicted
#label ANP\
105-121 #disulfide_bonds #status predicted
SUMMARY #length 128 #checksum 8741

Query Match 95.7%; Score 267; DB 2; Length 128;
Best Local Similarity 94.6%; Pred. No. 2.86e-42;
Matches 33; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Db 90 LRALLDAPSLRRSSCGFRMDRIGAQSLGCSNFRY 126
Qy 1 LRALLDAPSLRRSSCGFRMDRIGAQSLGCSNFRY 37

RESULT 8
ENTRY #type complete
TITLE atrial natriuretic factor precursor - rat
CONTAINS ANF(1-33); ANF(2-33); ANF(3-33); ANF(8-33); atrial
natriuretic peptide; atriopeptin I; atriopeptin II;
auriculin A; auriculin B; preprocardionatin
ORGANISM #formal_name Rattus norvegicus #common_name Norway rat
DATE 19-Feb-1984 #sequence_revision 15-Nov-1984 #text_change
26-Feb-1999
ACCESSIONS A22570; A01425; A93332; A43617; A93330; A94275; PT0061;
A20973; A44190; A60390; 159094; 158057; 152678
REFERENCE A22570
#authors Argentin, S.; Nemer, M.; Drouin, J.; Scott, G.K.; Kennedy,
B.P.; Davies, P.L.
#journal J. Biol. Chem. (1985) 260:4568-4571
#title The gene for rat atrial natriuretic factor.
```

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##cross-references MUID:85182558
#accession A22570
##molecule_type DNA
##residues 1-152 ##label ARG
##cross-references GB:K02062; NID:g202899; PID:g202900
REFERENCE A93331
#authors Yananaka, M.; Greenberg, B.; Johnson, L.; Seilhamer, J.;
Brewer, M.; Friedemann, T.; Miller, J.; Atlas, S.; Laragh,
J.; Lewicki, J.; Fiddes, J.
#journal Nature (1984) 309:719-722
#title Cloning and sequence analysis of the cDNA for the rat atrial
natriuretic factor precursor.
#cross-references MUID:84219797
#accession A01425
##molecule_type mRNA
##residues 1-152 ##label YAM
##cross-references EMBL:X00665; NID:g55711; PID:g55712
REFERENCE A93332
#authors Maki, M.; Takayanagi, R.; Misono, K.S.; Pandey, K.N.;
Tibbitts, C.; Inagami, T.
#journal Nature (1984) 309:724-724
#title Structure of rat atrial natriuretic factor precursor deduced
from cDNA sequence.
#cross-references MUID:84219798
#accession A93332
##molecule_type mRNA
##residues 1-152 ##label MAK
##cross-references GB:X00665; EMBL:X00658; NID:g55711; PID:g55712
REFERENCE A43617
#authors Seidman, C.E.; Duby, A.D.; Choi, E.; Graham, R.M.; Haber, E.;
Honey, C.; Smith, J.A.; Seidman, J.G.
#journal Science (1984) 225:324-326
#title The structure of rat preproatrial natriuretic factor as
defined by a complementary DNA clone.
#cross-references MUID:84250178
#accession A43617
##molecule_type mRNA
##residues 1-152 ##label SEI
##cross-references GB:K02062; GB:K02063; NID:g202899; PID:g202900
REFERENCE A93330
#authors Atlas, S.A.; Kleinert, H.D.; Camargo, M.J.; Januszewicz, A.;
Sealey, J.E.; Laragh, J.H.; Schilling, J.W.; Lewicki, J.A.;
Johnson, L.K.; Maack, T.
#journal Nature (1984) 309:717-719
#title Purification, sequencing and synthesis of natriuretic and
vasoactive rat atrial peptide.
#cross-references MUID:84219796
#accession A93330
##molecule_type protein
##residues 126-149 ##label ATL
REFERENCE A94275
#authors Currie, M.G.; Geller, D.M.; Cole, B.R.; Siegel, N.R.; Fox,
K.F.; Adams, S.P.; Eubanks, S.R.; Galluppi, G.R.;
Needleman, P.
#journal Science (1984) 223:67-69
#title Purification and sequence analysis of bioactive atrial
peptides (atriopeptins).
#cross-references MUID:84097513
#accession A94275
##molecule_type protein
##residues 127-149 ##label CUR
REFERENCE PT0061
#authors Thibault, G.; Murthy, K.K.; Gutkowska, J.; Seldah, N.G.;
Lazure, C.; Chretien, M.; Cantin, M.
#journal Peptides (1988) 9:47-53
#title NH2-terminal fragment of rat pro-atrial natriuretic factor in
the circulation: identification, radioimmunoassay and
half-life.
#cross-references MUID:88203350
#accession PT0061
##molecule_type protein
##residues 25-28,'X',30-31,'X',33,'X',35-38 ##label THI
REFERENCE A20973
```

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#authors      Seidah, N.G.; Lazure, C.; Chretien, M.; Thibault, G.; Garcia,
               R.; Cantin, M.; Genest, J.; Nutt, R.F.; Brady, S.F.; Lyle,
               T.A.; Paleveda, W.J.; Colton, C.D.; Ciccarone, T.M.; Veber,
               D.F.
#journal      Proc. Natl. Acad. Sci. U.S.A. (1984) 81:2640-2644
#title        Amino acid sequence of homologous rat atrial peptides:
               natriuretic activity of native and synthetic forms.
#cross-references MUID:84194062
#accession     A20973
#molecule_type mRNA
#residues      118-150 #label SE2
REFERENCE
#authors      Flynn, T.G.; Davies, P.L.; Kennedy, B.P.; de Bold, M.L.; de
               Bold, A.J.
#journal      Science (1985) 228:323-325
#title        Alignment of rat cardionatrin sequences with the
               preprocardionatrin sequence from complementary DNA.
#cross-references MUID:85168263
#accession     A44190
#molecule_type mRNA
#residues      1-152 #label FLY
#cross-references GB:K02062; NID:g202899; PID:g202900
#note         part of this sequence, including the amino ends of three
               mature peptides, was confirmed by protein sequencing
REFERENCE
#authors      Belcourt, D.; Varma, D.R.; Toney, K.; Bennett, H.P.J.
#journal      Protein Expr. Purif. (1990) 1:28-32
#title        Purification of rat pro-atrial natriuretic factor: a
               simplified scheme using reversed-phase high-performance
               liquid chromatography.
#cross-references MUID:93044510
#accession     A60390
#molecule_type protein
#residues      25-39 #label BEL
REFERENCE
#authors      Gardner, D.G.; Vlasuk, G.P.; Baxter, J.D.; Fiddes, J.C.;
               Lewicki, J.A.
#journal      Proc. Natl. Acad. Sci. U.S.A. (1987) 84:2175-2179
#title        Identification of atrial natriuretic factor gene transcripts
               in the central nervous system of the rat.
#cross-references MUID:87175636
#accession     I59094
#status        translated from GB/EMBL/DBJ
#molecule_type mRNA
#residues      38-152 #label RES
#cross-references GB:M15868; NID:g202903; PID:g202904
REFERENCE
#authors      Kangawa, K.; Tavaragi, Y.; Oikawa, S.; Mizuno, A.;
               Sakuragawa, Y.; Nakazato, H.; Fukuda, A.; Minamino, N.;
               Matsuo, H.
#journal      Nature (1984) 312:152-155
#title        Identification of rat gamma atrial natriuretic polypeptide
               and characterization of the cDNA encoding its precursor.
#cross-references MUID:85061500
#accession     I58057
#status        preliminary; translated from GB/EMBL/DBJ
#molecule_type mRNA
#residues      1-152 #label RE2
#cross-references EMBL:X01118; NID:g55716; PID:g55717
REFERENCE
#authors      Flynn, T.G.
#journal      Can. J. Physiol. Pharmacol. (1987) 65:2013-2020
#title        The elucidation of the structure of atrial natriuretic
               factor, a new peptide hormone.
#cross-references MUID:88109092
#accession     I52678
#status        preliminary; translated from GB/EMBL/DBJ
#molecule_type mRNA
#residues      1-51,'X',53-85,'X',87-152 #label RE3
#cross-references GB:M27498; NID:g202905; PID:g202906
COMMENT       A disulfide bond is required for full activity of atriopeptins.
               Several active peptides may be derived from the carboxyl region of
               this precursor.

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GENETICS
#gene          ANF
#introns       40/3; 149/3
CLASSIFICATION #superfamily natriuretic peptide A precursor
KEYWORDS       atrium; diuretic; hormone; natriuretic; osmoregulation
FEATURE        1-24
               #domain signal sequence #status predicted #label SIG\
               #product pro-atrial natriuretic factor #status
               experimental #label PRO\
25-152         #product cardionatrin IV #status experimental #label
               CN4\
25-150         #product cardionatrin III #status experimental #label
               CN3\
73-150         #product ANF(1-33) #status experimental #label ANF1\
               #product ANF(2-33) #status experimental #label ANF2\
               #product ANF(3-33) #status experimental #label ANF3\
               #product cardionatrin I #status experimental #label CN1\
               #product ANF(8-33) #status experimental #label ANF4\
               #product auriculin B #status experimental #label AUB\
               #product auriculin A #status experimental #label AUA\
               #product atrial natriuretic factor #status predicted
               #label MAT\
127-149        #product atriopeptin I #status experimental #label AT1\
127-147        #product atriopeptin II #status experimental #label AT2\
129-145        #disulfide_bonds #status experimental
SUMMARY        #length 152 #molecular-weight 16556 #checksum 7818
               Query Match 94.6%; Score 264; DB 1; Length 152;
               Best Local Similarity 91.9%; Pred. No. 1.49e-41;
               Matches 34; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Db 114 LRALLAGPSLRSSCFGRIDRIGAGSLGCNSFRY 150
QY 1 LRALLTAPSLRRSCFCGRMDRIGAGSLGCNSFRY 37
||||:|||||
RESULT 9
ENTRY   #type complete
TITLE   atrial natriuretic peptide precursor - mouse
ORGANISM #formal_name Mus musculus #common_name house mouse
DATE    31-Mar-1988 #sequence_revision 31-Mar-1988 #text_change
        20-Mar-1998
ACCESSION A29370; B43619
REFERENCE #authors Seidman, C.E.; Bloch, K.D.; Klein, K.A.; Smith, J.A.;
        #journal Science (1984) 226:1206-1209
        #title Nucleotide sequences of the human and mouse atrial
        #cross-references MUID:85065766
        #accession A29370
        #molecule_type DNA
        #residues 1-152 #label SEI
        #cross-references GB:K02781; NID:g191937; PID:g387099
GENETICS
#introns       40/3; 149/3
CLASSIFICATION #superfamily natriuretic peptide A precursor
KEYWORDS       atrium; diuretic; hormone; natriuretic; osmoregulation
FEATURE        1-24
               #domain signal sequence #status predicted #label SIG\
               #product gamma atrial natriuretic factor #status
               predicted #label ANF\
123-150        #product alpha atrial natriuretic peptide #status
               predicted #label ANP\
129-145        #disulfide_bonds #status predicted
SUMMARY        #length 152 #molecular-weight 16645 #checksum 9384
               Query Match 94.6%; Score 264; DB 1; Length 152;
               Best Local Similarity 91.9%; Pred. No. 1.49e-41;
               Matches 34; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Db 114 LRALLAGPSLRSSCFGRIDRIGAGSLGCNSFRY 150
||||:|||||

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```
QY 1 LRALLTAPRLRRSSCFGGMRDRIGAQSGLGCSNFRY 37

RESULT 10
ENTRY 155480 #type complete
TITLE hypothetical natriuretic peptide/phage fr coat protein mutant
ORGANISM fusion protein - synthetic
#note #formal_name Homo sapiens (man) and phage fr genes engineered and
expressed in Escherichia coli
DATE 02-Jul-1996 #sequence_revision 05-Sep-1996 #text_change
05-Sep-1996
ACCESSIONS 155480
REFERENCE 155480
#authors Berzins, V.; Jansone, I.; Skangals, A.; Kalnins, P.; Liepa,
S.; Baumanis, V.
#journal J. Biotechnol. (1993) 30:231-243
#title High level expression of alpha-human atrial natriuretic
factor as a fusion polypeptide with phage fr coat protein
in Escherichia coli.
#accession 155480
#status preliminary; translated from GB/EMBL/DBJ
#molecule_type DNA
#residues 1-161 #label RES
#cross-references GB:565657; NID:g435742; PID:g435743
KEYWORDS fusion protein
SUMMARY #length 161 #molecular-weight 17287 #checksum 337

Query Match 78.9%; Score 220; DB 4; Length 161;
Best Local Similarity 96.6%; Pred. No. 3.45e-31;
Matches 28; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Db 133 KSLRRSCFGGMRDRIGAQSGLGCSNFRY 161
:|||||:|||||:|||||:|||||:|||||:
QY 9 RSLRRSCFGGMRDRIGAQSGLGCSNFRY 37

RESULT 11
ENTRY JO0947 #type complete
TITLE atrial natriuretic peptide precursor - bullfrog
ALTERNATE_NAMES ANP; atrial natriuretic factor (ANF)
CONTAINS atrial natriuretic peptide-21; atrial natriuretic peptide-24
ORGANISM #formal_name Rana catesbeiana #common_name bullfrog
DATE 30-Sep-1991 #sequence_revision 30-Sep-1991 #text_change
20-Mar-1998
ACCESSIONS JO0947; A31510
REFERENCE JO0947
#authors Kojima, M.
#submission submitted to JIPID, May 1991
#accession JO0947
#molecule_type mRNA
#residues 1-145 #label KOJ
REFERENCE A31510
#authors Sakata, J.; Kangawa, K.; Matsuo, H.
#journal Biochem. Biophys. Res. Commun. (1988) 155:1338-1345
#title Identification of new atrial natriuretic peptides in frog
heart.
#cross-references MUID:89025806
#accession A31510
#molecule_type protein
#residues 122-145 #label SAK
COMMENT In mammals, several active peptides may be derived from the
prohormone.
CLASSIFICATION #superfamily natriuretic peptide A precursor
KEYWORDS atrium; diuretic; hormone; natriuretic; osmoregulation
FEATURE 1-23 #domain signal sequence #status predicted #label SIG\
24-121 #domain propeptide #status predicted #label PRO\
122-145 #product atrial natriuretic peptide-24 #status
experimental #label M24\
125-145 #product atrial natriuretic peptide-21 #status
experimental #label M21\
125-141 #disulfide_bonds #status predicted

SUMMARY #length 145 #molecular-weight 15934 #checksum 1892

Query Match 71.3%; Score 199; DB 2; Length 145;
Best Local Similarity 71.1%; Pred. No. 2.37e-26;
Matches 27; Conservative 5; Mismatches 4; Indels 2; Gaps 2;

Db 109 LRELLNAPRRSSDCFGSRIDRIGAQSGLGCSNFRY 145
|||:|||||:|||||:|||||:|||||:
QY 1 LRALLTAPRLRRSSCFGGMRDRIGAQSGLGCSNFRY 37

RESULT 12
ENTRY S01657 #type fragment
TITLE atrial natriuretic factor - laughing frog (fragment)
ALTERNATE_NAMES atriopeptin
ORGANISM #formal_name Rana ridibunda #common_name laughing frog
DATE 01-Dec-1989 #sequence_revision 01-Dec-1989 #text_change
09-Dec-1994
ACCESSIONS S01657; A30977
REFERENCE S01657
#authors Lazure, C.; Ong, H.; McNicoll, N.; Netchitallo, P.; Chretien,
M.; de Lean, A.; Vaudry, H.
#journal FEBS Lett. (1988) 238:300-306
#title The amino acid sequences of frog heart atrial
natriuretic-like peptide and mammalian ANF are closely
related.
#cross-references MUID:89005705
#accession S01657
#molecule_type protein
#residues 1-30 #label LAZ
#note the sequence from the summary is inconsistent with that
from Fig. 3 in lacking residues 3-6
CLASSIFICATION #superfamily natriuretic peptide A precursor
SUMMARY #length 30 #checksum 4650

Query Match 61.6%; Score 172; DB 2; Length 30;
Best Local Similarity 76.7%; Pred. No. 2.85e-20;
Matches 23; Conservative 4; Mismatches 2; Indels 1; Gaps 1;

Db 1 APRSMRRSSDCFGSRIDRIGAQSGLGCSNFRY 30
|||||:|||||:|||||:|||||:
QY 7 APRSLRRSSCFGGMRDRIGAQSGLGCSNFRY 35
|||||:|||||:|||||:|||||:

RESULT 13
ENTRY A41403 #type complete
TITLE aldosterone secretion inhibitory factor precursor - bovine
ORGANISM #formal_name Bos primigenius taurus #common_name cattle
DATE 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change
03-Mar-1995
ACCESSIONS A41403; A30976
REFERENCE A41403
#authors Nguyen, T.T.; Lazure, C.; Babinski, K.; Chretien, M.; De
Lean, A.; Ong, H.
#journal Mol. Endocrinol. (1989) 3:1823-1829
#title Purification and primary structure of pro-aldosterone
secretion inhibitory factor from bovine adrenal chromaffin
cells.
#cross-references MUID:90114187
#accession A41403
#molecule_type protein
#residues 1-103 #label NGU
REFERENCE A30976
#authors Nguyen, T.T.; Lazure, C.; Babinski, K.; Chretien, M.; Ong,
H.; de Lean, A.
#journal Endocrinology (1989) 124:1591-1593
#title Aldosterone secretion inhibitory factor: a novel neuropeptide
in bovine chromaffin cells.
#cross-references MUID:89136947
#accession A30976
#molecule_type protein
#residues 69-103 #label NG2
CLASSIFICATION #superfamily natriuretic peptide A precursor
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SUMMARY          #length 103 #molecular-weight 11249 #checksum 7671
Query Match      57.3%; Score 160; DB 2; Length 103;
Best Local Similarity 60.5%; Pred. No. 1.25e-17;
Matches 23; Conservative 7; Mismatches 6; Indels 2; Gaps 2;

Db 67 LRAL-RGPKMRDSCFGRRLDRIGSLGSLGCNVLRYY 103
|||| :|:| :|:| :|:| :|:| :|:| :|:| :|:| :|:|
QY 1 LRALLTAPRSLRRSSCFGRMDRIGAQSGLCNSFR-Y 37

RESULT 14
ENTRY
TITLE          A33873      #type complete
ORGANISM       brain natriuretic peptide precursor - pig
DATE           #formal_name Sus scrofa domestica #common_name domestic pig
               #formal_name Sus scrofa domestica #common_name domestic pig
               27-Feb-1990 #sequence_revision 27-Feb-1990 #text_change
               29-Jan-1999
ACCESSIONS     A33873; A31675
REFERENCE      A33873
#authors       Porter, J.G.; Arfsten, A.; Palisi, T.; Scarborough, R.M.;
               Lewicki, J.A.; Seilhamer, J.J.
#journal       J. Biol. Chem. (1989) 264:6689-6692
#title         Cloning of a cDNA encoding porcine brain natriuretic peptide.
#cross-references MUID:89214071
#accession     A33873
#status        preliminary
#molecule_type mRNA
#residues      1-131 #label POR
#cross-references GB:M25547; GB:J04708; GB:M22477; GB:M22478;
               NID:g164392; PID:g164393

REFERENCE      A31675
#authors       Minamino, N.; Kangawa, K.; Matsuo, H.
#journal       Biochem. Biophys. Res. Commun. (1988) 157:402-409
#title         Isolation and identification of a high molecular weight brain
               natriuretic peptide in porcine cardiac atrium.
#cross-references MUID:89061743
#accession     A31675
#status        preliminary
#molecule_type protein
#residues      26-131 #label MIN
CLASSIFICATION #superfamily natriuretic peptide A precursor
SUMMARY        #length 131 #molecular-weight 14512 #checksum 2829

Query Match      56.3%; Score 157; DB 2; Length 131;
Best Local Similarity 55.3%; Pred. No. 5.61e-17;
Matches 21; Conservative 10; Mismatches 5; Indels 2; Gaps 2;

Db 95 LRGI-RSPKTRDSCFGRRLDRIGSLGSLGCNVLRYY 131
|||| :|:| :|:| :|:| :|:| :|:| :|:| :|:| :|:|
QY 1 LRALLTAPRSLRRSSCFGRMDRIGAQSGLCNSFR-Y 37

RESULT 15
ENTRY
TITLE          A31676      #type complete
ALTERNATE_NAMES brain natriuretic factor precursor - pig
ORGANISM       brain natriuretic factor 32
DATE           #formal_name Sus scrofa domestica #common_name domestic pig
               21-May-1990 #sequence_revision 21-May-1990 #text_change
               29-Jan-1999
ACCESSIONS     A31676; A31517; S06359
REFERENCE      A31676
#authors       Maekawa, K.; Sudoh, T.; Furusawa, M.; Minamino, N.; Kangawa,
               K.; Ohkubo, H.; Nakanishi, S.; Matsuo, H.
#journal       Biochem. Biophys. Res. Commun. (1988) 157:410-416
#title         Cloning and sequence analysis of cDNA encoding a precursor
               for porcine brain natriuretic peptide.
#cross-references MUID:89061744
#accession     A31676
#molecule_type mRNA
#residues      1-131 #label MAE
#cross-references GB:M23596; NID:g535704; PID:g535705
REFERENCE      A31517
#authors       Sudoh, T.; Minamino, N.; Kangawa, K.; Matsuo, H.
```

```
#journal         Biochem. Biophys. Res. Commun. (1988) 155:726-732
#title           Brain natriuretic peptide-32: N-terminal six amino acid
               extended form of brain natriuretic peptide identified in
               porcine brain.
#cross-references MUID:88339957
#accession       A31517
#molecule_type protein
#residues        100-131 #label SUD
REFERENCE        S06359
#authors         Sudoh, T.; Kangawa, K.; Minamino, N.; Matsuo, H.
#journal         Nature (1988) 332:78-81
#title           A new natriuretic peptide in porcine brain.
#cross-references MUID:88156915
#accession       S06359
#molecule_type protein
#residues        106-131 #label SU2
CLASSIFICATION  #superfamily natriuretic peptide A precursor
KEYWORDS         brain; natriuretic
FEATURE
1-25             #domain signal sequence #status predicted #label SIG\
26-131          #product brain gamma natriuretic factor #status
               predicted #label GAM\
100-131         #product brain alpha natriuretic peptide #status
               experimental #label ALF\
109-125         #disulfide_bonds #status experimental
SUMMARY          #length 131 #molecular-weight 14538 #checksum 3271

Query Match      56.3%; Score 157; DB 2; Length 131;
Best Local Similarity 55.3%; Pred. No. 5.61e-17;
Matches 21; Conservative 10; Mismatches 5; Indels 2; Gaps 2;

Db 95 LRGI-RSPKTRDSCFGRRLDRIGSLGSLGCNVLRYY 131
|||| :|:| :|:| :|:| :|:| :|:| :|:| :|:| :|:|
QY 1 LRALLTAPRSLRRSSCFGRMDRIGAQSGLCNSFR-Y 37

Search completed: Wed Jun 16 12:49:28 1999
Job time : 31 secs.
```

WQESRLH

(TM)

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MPsrch_pp protein - protein database search, using Smith-Waterman algorithm

Run on: Wed Jun 16 12:49:46 1999; MasPar time 3.22 Seconds
324.910 Million cell updates/sec
Tabular output not generated.

Title: >VANDER-027-213.PEP
Description: (1-37) from vander027777.pep
Perfect Score: 279
Sequence: 1 LRALLTAPSLRRSSCFGMDRIGASGLGCSNFRY 37

Scoring table: PAM 150
Gap 11

Searched: 77977 seqs, 28268293 residues

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database: swiss-prot37
1:swissprot

Statistics: Mean 33.663; Variance 47.480; scale 0.709

pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description	Pred. No.
1	279	100.0	152	1	ANF_BOVIN	2.07e-51
2	279	100.0	153	1	ANF_HUMAN	2.07e-51
3	276	98.9	149	1	ANF_CANFA	1.36e-50
4	276	98.9	150	1	ANF_PIG	1.36e-50
5	276	98.9	153	1	ANF_HORSE	1.36e-50
6	270	96.8	153	1	ANF_RABIT	5.80e-49
7	267	95.7	128	1	ANF_CAVPO	3.77e-48
8	264	94.6	152	1	ANF_MOUSE	2.45e-47
9	264	94.6	152	1	ANF_RAT	2.45e-47
10	199	71.3	145	1	ANF_CANFA	4.13e-30
11	172	61.6	30	1	ANF_RANRI	3.12e-23
12	160	57.3	103	1	ANF_BOVIN	3.01e-20
13	157	56.3	131	1	ANF_PIG	1.65e-19
14	155	55.6	141	1	ANF_CANFA	5.09e-19
15	143	51.3	140	1	ANF_CHICK	4.08e-16
16	131	47.0	36	1	ANFV_ANGJA	2.79e-13
17	129	46.2	134	1	ANF_HUMAN	8.16e-13
18	124	44.4	127	1	ANF_ANGJA	1.16e-11
19	118	42.3	121	1	ANF_RAT	2.67e-10
20	114	40.9	122	1	ANF_CHICK	2.10e-09
21	112	40.1	131	1	ANFV_ANGJA	5.81e-09
22	107	38.4	115	1	ANFV_TRISC	7.21e-08
23	107	38.4	115	1	ANFV_SCICA	7.21e-08

24	107	38.4	126	1	ANFC_RAT	C-TYPE NATRIURETIC PEP	7.21e-08
25	107	38.4	126	1	ANFC_PIG	C-TYPE NATRIURETIC PEP	7.21e-08
26	107	38.4	126	1	ANFC_SHEEP	C-TYPE NATRIURETIC PEP	7.21e-08
27	107	38.4	126	1	ANFC_BOVIN	C-TYPE NATRIURETIC PEP	7.21e-08
28	107	38.4	126	1	ANFC_HUMAN	C-TYPE NATRIURETIC PEP	7.21e-08
29	107	38.4	126	1	ANFC_MOUSE	C-TYPE NATRIURETIC PEP	7.21e-08
30	107	38.4	135	1	ANFC_SQUAC	C-TYPE NATRIURETIC PEP	7.21e-08
31	106	38.0	121	1	ANFB_MOUSE	BRAIN NATRIURETIC PEP	1.19e-07
32	104	37.3	118	1	ANFD_RANCA	C-TYPE NATRIURETIC PEP	3.20e-07
33	102	36.6	129	1	ANFC_RANCA	C-TYPE NATRIURETIC PEP	8.53e-07
34	92	33.0	38	1	DNP_DENAN	NATRIURETIC PEPTIDE (D	1.02e-04
35	78	28.0	763	1	PSRA_WOLSU	POLYSULFIDE REDUCTASE	5.23e-02
36	74	26.5	639	1	TETM_STRLI	TETRACYCLINE RESISTANC	2.77e-01
37	74	26.5	476	1	EPAL_HUMAN	EPHRIN TYPE-A RECEPT	9.30e-01
38	71	25.4	383	1	CYSLSVPII	SERINE/THREONINE-PROTE	1.38e+00
39	70	25.1	404	1	YK33_YEAST	HYPOHETICAL 46.5 KD P	1.38e+00
40	70	25.1	550	1	ID5_HUMAN	IDURONATE 2-SULFATASE	1.38e+00
41	70	25.1	683	1	EFG1_TREPA	ELONGATION FACTOR G 1	1.38e+00
42	69	24.7	857	1	V2A_CMVY	PROBABLE RNA-DIRECTED	2.04e+00
43	69	24.7	857	1	V2A_CMVFN	PROBABLE RNA-DIRECTED	2.04e+00
44	69	24.7	858	1	V2A_CMVVK	PROBABLE RNA-DIRECTED	2.04e+00
45	69	24.7	858	1	V2A_CMVVK	PROBABLE RNA-DIRECTED	2.04e+00

ALIGNMENTS

RESULT 1
ID ANF_BOVIN STANDARD; PRT; 152 AA.
AC P07501;
DT 01-APR-1988 (REL. 07, CREATED)
DT 01-MAR-1989 (REL. 10, LAST SEQUENCE UPDATE)
DT 01-OCT-1996 (REL. 34, LAST ANNOTATION UPDATE)
DE ATRIAL NATRIURETIC FACTOR PRECURSOR (ANF) (ATRIAL NATRIURETIC PEPTIDE)
DE (ANP) (PREPONTATRIODILATIN).
GN NPFA.
OS BOS TAURUS (BOVINE).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA;
OC ARTIODACTYLA; RUMINANTIA; PECORA; BOVIDAE; BOVINAE; BOS.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE; 86215205.
RA VLASUK G.P., MILLER J., BENEN G.H., LEWICKI J.A.;
RT "Structure and analysis of the bovine atrial natriuretic peptide
RT precursor gene.";
RL BIOCHEM. BIOPHYS. RES. COMMUN. 136:396-403(1986).
RN [2]
RP SEQUENCE OF 123-150.
RX MEDLINE; 86173941.
RA ONG H., MCNICOLL N., LAZURE C., SEIDAH N., CHRETIEN M., CANTIN M.,
RA DE LEAN A.;
RT "Purification and sequence determination of bovine atrial natriuretic
RT factor.";
CC LIFE SCI. 38:1309-1315(1986).
CC -1- FUNCTION: ATRIAL NATRIURETIC FACTOR (ANF) IS A POTENT VASOACTIVE
CC SUBSTANCE SYNTHESIZED IN MAMMALIAN ATRIA AND IS THOUGHT TO PLAY A
CC KEY ROLE IN CARDIOVASCULAR HOMEOSTASIS. HAS A CGMP-STIMULATING
CC ACTIVITY.
CC -1- A DISULFIDE BOND IS REQUIRED FOR FULL ACTIVITY OF ATRIOPEPTINS.
CC -1- SIMILARITY: BELONGS TO THE NATRIURETIC PEPTIDES FAMILY.
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; M13145; G162666; -
CC PIR; A24247; AWBO.
CC PROSITE; PSC0263; NATRIURETIC_PEPTIDE; 1.
CC PFAM; PF00212; ANP; 1.
CC VASOACTIVE; SIGNAL.

"Molecular cloning and characterization of DNA sequences encoding rat and human atrial natriuretic factors.";
PROC. NATL. ACAD. SCI. U.S.A. 81:6325-6329(1984).
[8]
SEQUENCE OF 1-75 FROM N.A.
RX MEDLINE; 85095983.
RX MAKI M., PARMENTIER M., INAGAMI T.;
RT "Cloning of genomic DNA for human atrial natriuretic factor.";
RT BIOCHEM. BIOPHYS. RES. COMMUN. 125:797-802(1984).
[9]
SEQUENCE OF 124-151.
RX MEDLINE; 84128019.
RX KANGAWA K., MATSUO H.;
RT "Purification and complete amino acid sequence of alpha-human atrial
RT natriuretic polypeptide (alpha-hANP).";
RL BIOCHEM. BIOPHYS. RES. COMMUN. 118:131-139(1984).
[10]
STRUCTURE BY NMR OF 124-151 MUTANT SELECTIVE FOR NPR-C RECEPTOR.
RX MEDLINE; 94318633.
RX FAIRBROTHER W.J., MCDOWELL R.S., CUNNINGHAM B.C.;
RT "Solution conformation of an atrial natriuretic peptide variant
RT selective for the type A receptor.";
RL BIOCHEMISTRY 33:8897-8904(1994).
CC -!- FUNCTION: ATRIAL NATRIURETIC FACTOR (ANF) IS A POTENT VASOACTIVE
CC SUBSTANCE SYNTHESIZED IN MAMMALIAN ATRIA AND IS THOUGHT TO PLAY A
CC KEY ROLE IN CARDIOVASCULAR HOMEOSTASIS. HAS A CGMP-STIMULATING
CC ACTIVITY.
CC -!- THE HUMAN GENOME CONTAINS 2 DIFFERENT PREPRONATRIODILATIN GENES
CC ONE CODES FOR 2 ARG RESIDUES AT THE C-TERMINUS THAT ARE CLEAVED
CC TO FORM THE MATURE PEPTIDE, WHILE THE OTHER ENDS IN A TERMINATION
CC CODON IMMEDIATELY AFTER THE LAST CODON OF THE MATURE PEPTIDE.
CC -!- SIMILARITY: BELONGS TO THE NATRIURETIC PEPTIDES FAMILY.
CC -----
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CC -----
EMBL; X01470; G825625; -
EMBL; X02558; G825625; JOINED.
EMBL; K02043; G178630; -
EMBL; X01471; E27452; ALT_SEQ.
EMBL; K02044; G178632; -
EMBL; A021155; E1294859; -
EMBL; M30262; G180182; -
EMBL; K02399; G178634; -
PIR; A01424; AWHU
PIR; A22693; A22693.
PIR; A32733; A32733.
PDB; 1ANP; 07-APR-95.
MIM; 108780; -
DR PROSITE; P500263; NATRIURETIC_PEPTIDE; 1.
DR PFAM; PF00212; ANP; 1.
KW VASOACTIVE; SIGNAL; 3D-STRUCTURE.
FT SIGNAL
FT 1 25
FT PEPTIDE 26 55
FT PEPTIDE 124 151
FT DISULFID 130 146
FT VARIANT 152 153
FT SEQUENCE 153 AA; 16708 MW; C24A68AF CRC32;
SQ

Query Match 100.0%; Score 279; DB 1; Length 153;
Best Local Similarity 100.0%; Pred. No. 2.07e-51;
Matches 37; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 115 LRALLTAPSLRSSCGGGRMDRIGAQSGILGCSNFRY 151
QY 1 LRALLTAPSLRSSCGGGRMDRIGAQSGILGCSNFRY 37

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CC EMBL: X58563; G1009; -
DR PIR: S14873; S14873.
DR PROSITE: PS00263; NATRIURETIC_PEPTIDE; 1.
DR PFAM: PF00212; ANP; 1.
KW VASOACTIVE; SIGNAL. 25
FT SIGNAL 1 25 POTENTIAL.
FT PEPTIDE 124 151 ATRIAL NATRIURETIC PEPTIDE, ALPHA (ANP).
FT DISULFID 130 146 BY SIMILARITY.
SQ SEQUENCE 153 AA; 16825 MW; FESD5F4A CRC32;

Query Match 98.9%; Score 276; DB 1; Length 153;
Best Local Similarity 97.3%; Pred. No. 1.36e-50;
Matches 36; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Db 115 LRALLAPRSLRRSCFGGRMDRIGAGSLGCSNFRY 151
Qy 1 LRALLAPRSLRRSCFGGRMDRIGAGSLGCSNFRY 37

RESULT 6
ID ANF_RABBIT STANDARD; PRT; 153 AA.
AC P07500.
DT 01-APR-1988 (REL. 07, CREATED)
DT 01-APR-1988 (REL. 07, LAST SEQUENCE UPDATE)
DT 01-OCT-1996 (REL. 34, LAST ANNOTATION UPDATE)
DE ATRIAL NATRIURETIC FACTOR PRECURSOR (ANF) (ATRIAL NATRIURETIC PEPTIDE)
DE (ANP) (PREPRONATRIODILATIN).
GN NPFA.

OS ORYCTOLAGUS CUNICULUS (RABBIT).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA;
OC LAGOMORPHA; LEPORIDAE; ORYCTOLAGUS.
RN [1]

RP SEQUENCE FROM N.A.
RX MEDLINE: 86076957.
RA OIKAWA S., IMAI M., INUZUKA C., TANABAGI Y., NAKAZATO H., MATSUO H.;
RT "Structure of dog and rabbit precursors of atrial natriuretic
RL POLYPEPTIDES deduced from nucleotide sequence of cloned cDNA.";
RL BIOCHEM. BIOPHYS. RES. COMMUN. 132:892-899(1985).
CC -!- FUNCTION: ATRIAL NATRIURETIC FACTOR (ANF) IS A POTENT VASOACTIVE
CC SUBSTANCE SYNTHESIZED IN MAMMALIAN ATRIA AND IS THOUGHT TO PLAY A
CC KEY ROLE IN CARDIOVASCULAR HOMEOSTASIS. HAS A CGMP-STIMULATING
CC ACTIVITY.

CC -!- A DISULFIDE BOND IS REQUIRED FOR FULL ACTIVITY OF ATRIOPEPTINS.
CC -!- SIMILARITY: BELONGS TO THE NATRIURETIC PEPTIDES FAMILY.
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CC EMBL: M12046; G164771; -
DR PIR: B25302; AWRB.
DR PROSITE: PS00263; NATRIURETIC_PEPTIDE; 1.
DR PFAM: PF00212; ANP; 1.
KW VASOACTIVE; SIGNAL. 25
FT SIGNAL 1 25
FT PEPTIDE 124 151 ATRIAL NATRIURETIC PEPTIDE, ALPHA (ANP).
FT DISULFID 130 146
SQ SEQUENCE 153 AA; 16843 MW; 1FA4FB42 CRC32;

Query Match 96.8%; Score 270; DB 1; Length 153;
Best Local Similarity 97.3%; Pred. No. 5.80e-49;
Matches 36; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Db 115 LRALLAPRSLRRSCFGGRMDRIGAGSLGCSNFRY 151
Qy 1 LRALLAPRSLRRSCFGGRMDRIGAGSLGCSNFRY 37

RESULT 7
ID ANF_CAVPO STANDARD; PRT; 128 AA.
AC P27596.
DT 01-AUG-1992 (REL. 23, CREATED)
DT 01-AUG-1992 (REL. 23, LAST SEQUENCE UPDATE)
DT 01-OCT-1996 (REL. 34, LAST ANNOTATION UPDATE)
DE ATRIAL NATRIURETIC FACTOR PRECURSOR (ANF) (ATRIAL NATRIURETIC PEPTIDE)
DE (ANP) (PREPRONATRIODILATIN) (FRAGMENT).
GN NPFA.

OS CAVIA PORCELLUS (GUINEA PIG).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA;
OC RODENTIA; HYSTRICOGNATHI; CAVIIDAE; CAVIA.
RN [1]

RP SEQUENCE FROM N.A.
RC TISSUE=HEART ATRIUM;
RA MARGERT H.J., HANKE M., SCHMEDING G., TEUTEBERG K.,
RL SCHULZ-KNAPPE P., FORSSMANN W.G.;
RL SUBMITTED (MAR-1991) TO EMBL/GENBANK/DBJ DATA BANKS.

CC -!- FUNCTION: ATRIAL NATRIURETIC FACTOR (ANF) IS A POTENT VASOACTIVE
CC SUBSTANCE SYNTHESIZED IN MAMMALIAN ATRIA AND IS THOUGHT TO PLAY A
CC KEY ROLE IN CARDIOVASCULAR HOMEOSTASIS. HAS A CGMP-STIMULATING
CC ACTIVITY.

CC -!- DEVELOPMENTAL STAGE: ADULT.
CC -!- A DISULFIDE BOND IS REQUIRED FOR FULL ACTIVITY OF ATRIOPEPTINS.
CC -!- SIMILARITY: BELONGS TO THE NATRIURETIC PEPTIDES FAMILY.
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CC EMBL: X58562; G49544; -
DR PIR: S14872; S14872.
DR PROSITE: PS00263; NATRIURETIC_PEPTIDE; 1.
DR PFAM: PF00212; ANP; 1.
KW VASOACTIVE.
FT NON_TER 1 1
FT PEPTIDE 1 30 CARDIODILATIN-RELATED PEPTIDE (CDP).
FT PEPTIDE 99 126 ATRIAL NATRIURETIC PEPTIDE, ALPHA (ANP).
FT DISULFID 105 121 BY SIMILARITY.
SQ SEQUENCE 128 AA; 13366 MW; 2C2F552D CRC32;

Query Match 95.7%; Score 267; DB 1; Length 128;
Best Local Similarity 94.6%; Pred. No. 3.77e-48;
Matches 35; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Db 90 LRALLAPRSLRRSCFGGRMDRIGAGSLGCSNFRY 126
Qy 1 LRALLAPRSLRRSCFGGRMDRIGAGSLGCSNFRY 37

RESULT 8
ID ANF_RAT STANDARD; PRT; 152 AA.
AC P01161.
DT 21-JUL-1986 (REL. 01, CREATED)
DT 21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)
DT 15-DEC-1998 (REL. 37, LAST ANNOTATION UPDATE)
DE ATRIAL NATRIURETIC FACTOR PRECURSOR (ANF) (ATRIAL NATRIURETIC PEPTIDE)
DE (ANP) (PREPRONATRIODILATIN) [CONTAINS: AURICULINS; ATRIOPEPTINS].
GN NPFA.

OS RATTUS NORVEGICUS (RAT).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA;
OC RODENTIA; SCIUROGNATHI; MURIDAE; MURINAE; RATTUS.
RN [1]
RP SEQUENCE FROM N.A.

RA MEDLINE: 84219797.
RA YAMAKA M., GRENBORG B., JOHNSON L., SEILHAMER J.J., BREWER M.,
RA FRIEDMANN T., MILLER J., ATLAS S.A., LARAGH J., LEWICKI J.,
RA FIDDES J.C.;
RT "Cloning and sequence analysis of the cDNA for the rat atrial
RT natriuretic factor precursor.";
RL NATURE 309:719-722(1984).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE: 84219798.
RA MAKI M., TAKAYANAGI R., MISONO K.S., PANDEY K.N., TIBBETTS C.,
RA INAGAMI T.;
RT "Structure of rat atrial natriuretic factor precursor deduced from
RT cDNA sequence.";
RL NATURE 309:722-724(1984).
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE: 84250178.
RA SEIDMAN C.E., DUBY A.D., CHOI E., GRAHAM R.M., HABER E., HOMCY C.,
RA SMITH J.A., SEIDMAN J.G.;
RT "The structure of rat preproatrial natriuretic factor as defined by a
RT complementary DNA clone.";
RL SCIENCE 225:324-326(1984).
RN [4]
RP SEQUENCE FROM N.A.
RX MEDLINE: 85061500.
RA KANGAWA K., TAWARAGI Y., OIKAWA S., MIZUNO A., SAKURAGAWA Y.,
RA KANAZATO H., FUKUDA A., MINAMINO N., MATSUO H.;
RT "Identification of rat gamma atrial natriuretic polypeptide and
RT characterization of the cDNA encoding its precursor.";
RL NATURE 312:152-155(1984).
RN [5]
RP SEQUENCE FROM N.A.
RX MEDLINE: 85182558.
RA ARGENTIN S., NEMER M., DROUIN J., SCOTT G.K., KENNEDY B.P.,
RA DAVIES P.L.;
RT "The gene for rat atrial natriuretic factor.";
RL J. BIOL. CHEM. 260:4568-4571(1985).
RN [6]
RP SEQUENCE FROM N.A.
RX MEDLINE: 85038509.
RA ZIVIN R.A., CONDRA J.H., DIXON R.A.F., SEIDAH N.G., CHRETIEN M.,
RA NEMER M., CHAMBERLAND M., DROUIN J.;
RT "Molecular cloning and characterization of DNA sequences encoding rat
RT and human atrial natriuretic factors.";
RL PROC. NATL. ACAD. SCI. U.S.A. 81:6325-6329(1984).
RN [7]
RP SEQUENCE FROM N.A.
RX MEDLINE: 88109092.
RA FLYNN T.G.;
RT "The elucidation of the structure of atrial natriuretic factor, a new
RT peptide hormone.";
RL CAN. J. PHYSIOL. PHARMACOL. 65:2013-2020(1987).
RN [8]
RP SEQUENCE OF 38-152 FROM N.A.
RX MEDLINE: 8715636.
RA GARDNER D.G., VLASUK G.P., BAXTER J.D., FIDDES J.C., LEWICKI J.A.;
RT "Identification of atrial natriuretic factor gene transcripts in the
RT central nervous system of the rat.";
RL PROC. NATL. ACAD. SCI. U.S.A. 84:2175-2179(1987).
RN [9]
RP AURICULINS, SEQUENCE, AND SYNTHESIS OF 126-149.
RX MEDLINE: 84219796.
RA ATLAS S.A., KLEINERT H.D., CAMARGO M.J., JANUSZEWICZ A., SEALEY J.E.,
RA LARAGH J.H., SCHILLING J.W., LEWICKI J.A., JOHNSON L.K., MAACK T.;
RT "Purification, sequencing and synthesis of natriuretic and vasoactive
RT rat atrial peptide.";
RL NATURE 309:717-719(1984).
RN [10]
RP SEQUENCE OF 127-149, AND SYNTHESIS.
RX MEDLINE: 84097513.
RA CURRIE M.G., GELLER D.M., COLE B.R., SIEGEL N.R., FOK K.F.,
RA ADAMS S.P., EUBANKS S.R., GALLUPPI G.R., NEEDLEMAN P.;

RT "Purification and sequence analysis of bioactive atrial peptides
RT (atriopeptins).";
RL SCIENCE 223:67-69(1984).
RN [11]
RP SEQUENCE OF 118-150.
RX MEDLINE: 84194062.
RA SEIDAH N.G., LAZURE C., CHRETIEN M., THIBAUT G., GARCIA R.,
RA CANTIN M., GINEST J., NUTT R.F., BRADY S.F., LYLE T.A., PALEVEDA W.J.,
RA COLTON C.D., CICCARONE T.M., VEBER D.F.;
RT "Amino acid sequence of homologous rat atrial peptides: natriuretic
RT activity of native and synthetic forms.";
RL PROC. NATL. ACAD. SCI. U.S.A. 81:2640-2644(1984).
RN [12]
RP SEQUENCE OF 25-38.
RX MEDLINE: 88203350.
RA THIBAUT G., MURTHY K.K., GUTKOWSKA J., SEIDAH N.G., LAZURE C.,
RA CHRETIEN M., CANTIN M.;
RT "NH2-terminal fragment of rat pro-atrial natriuretic factor in the
RT circulation: identification, radioimmunoassay and half-life.";
RL PEPTIDES 9:47-53(1988).
CC -1- FUNCTION: ATRIAL NATRIURETIC FACTOR (ANF) IS A POTENT VASOACTIVE
CC SUBSTANCE SYNTHESIZED IN MAMMALIAN ATRIA AND IS THOUGHT TO PLAY A
CC KEY ROLE IN CARDIOVASCULAR HOMEOSTASIS. HAS A CGMP-STIMULATING
CC ACTIVITY.
CC -1- A DISULFIDE BOND IS REQUIRED FOR FULL ACTIVITY OF ATRIOPEPTINS.
CC -1- SIMILARITY: BELONGS TO THE NATRIURETIC PEPTIDES FAMILY.
CC
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CC
CC EMBL: M15868; G202904;
CC EMBL: X00665; G55712;
CC EMBL: X02062; G202900;
CC EMBL: X01118; G55717;
CC EMBL: M27498; G202906;
CC PIR: A22570; AWRT.
CC PIR: A44190; A44190.
CC PROSITE: PS00263; NATRIURETIC_PEPTIDE; 1.
CC PFAM: PF00212; ANP; 1.
CC KW VASOACTIVE; SIGNAL.
CC FT SIGNAL 1 24
CC FT PEPTIDE 126 149 AURICULIN A.
CC FT PEPTIDE 126 150 AURICULIN B.
CC FT PEPTIDE 127 147 ATRIOPEPTIN I.
CC FT PEPTIDE 127 149 ATRIOPEPTIN II.
CC FT PEPTIDE 127 150 ATRIOPEPTIN III.
CC FT DISULFID 129 145
CC SEQUENCE 152 AA; 16556 MW; 2D424B75 CRC32;
SQ
Query Match 94.6%; Score 264; DB 1; Length 152;
Best Local Similarity 91.9%; Pred. No. 2.45e-47;
Matches 34; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
Db 114 LRALLAGPRLRRSSCFGRIDRIGAGQSLGNCSPRY 150
QY 1 LRALLTAPRLRRSSCFGRGMDRIGAGQSLGNCSPRY 37
RESULT 9
ID ANF_MOUSE STANDARD; PRT; 152 AA.
AC P05125;
DT 13-AUG-1987 (REL. 05, CREATED)
DT 13-AUG-1987 (REL. 05, LAST SEQUENCE UPDATE)
DT 01-OCT-1996 (REL. 34, LAST ANNOTATION UPDATE)
DE ATRIAL NATRIURETIC FACTOR PRECURSOR (ANF) (ATRIAL NATRIURETIC PEPTIDE)
DE (ANF) (PREPRONATRIODILATIN).
GN NPFA OR PND.
OS MUS MUSCULUS (MOUSE).

CC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA;
 CC ROENTHIA; SCIUROGNATHI; MURIDAE; MURINAE; MUS.
 RN (1)
 RP SEQUENCE FROM N.A.
 RA MEDLINE; 85065766.
 RX SEIDMAN C.E., BLOCH K.D., KLEIN K.A., SMITH J.A., SEIDMAN J.G.;
 RT "Nucleotide sequences of the human and mouse atrial natriuretic
 factor genes";
 RL SCIENCE 226:1206-1209(1984).
 CC -1- FUNCTION: ATRIAL NATRIURETIC FACTOR (ANF) IS A POTENT VASOACTIVE
 CC SUBSTANCE SYNTHESIZED IN MAMMALIAN ATRIA AND IS THOUGHT TO PLAY A
 CC KEY ROLE IN CARDIOVASCULAR HOMEOSTASIS. HAS A CGMP-STIMULATING
 CC ACTIVITY.
 CC -1- A DISULFIDE BOND IS REQUIRED FOR FULL ACTIVITY OF ATRIOPEPTINS.
 CC -1- SIMILARITY: BELONGS TO THE NATRIURETIC PEPTIDES FAMILY.
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 CC -----
 CC EMBL; K02781; G387099; ..
 DR PIR: A29370; AMWS.
 DR MGI: 97367; NPPA.
 DR PROSITE; PS00263; NATRIURETIC_PEPTIDE; 1.
 DR PFAM; PF00212; ANP; 1.
 KW VASOACTIVE; SIGNAL.
 FT SIGNAL 1 24
 FT PEPTIDE 126 149 AURICULIN A (BY SIMILARITY).
 FT PEPTIDE 126 150 AURICULIN B (BY SIMILARITY).
 FT PEPTIDE 127 149 ATRIOPEPTIN I (BY SIMILARITY).
 FT PEPTIDE 127 147 ATRIOPEPTIN II (BY SIMILARITY).
 FT DISULFID 129 145 BY SIMILARITY.
 SQ SEQUENCE 152 AA; 16645 MW; 5163CB23 CRC32;
 Query Match 94.6%; Score 264; DB 1; Length 152;
 Best Local Similarity 91.9%; Pred. No. 2.45e-47;
 Matches 34; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
 Db 114 LRALLAPRSLRSSCFGGRMDRIGAQSGLCNSFRY 150
 QY 1 LRALLAPRSLRSSCFGGRMDRIGAQSGLCNSFRY 37
 RESULT 10
 ID ANF_RANCA STANDARD; PRT: 145 AA.
 AC P18509;
 DT 01-NOV-1990 (REL. 16, CREATED)
 DT 01-NOV-1992 (REL. 21, LAST SEQUENCE UPDATE)
 DT 01-FEB-1995 (REL. 31, LAST ANNOTATION UPDATE)
 DE ATRIAL NATRIURETIC FACTOR PRECURSOR (ANF) (ATRIAL NATRIURETIC PEPTIDE)
 DE (ANP).
 OS RANA CATESBEIANA (BULL FROG).
 CC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; AMPHIBIA; BATRACHIA; ANURA;
 CC NEOBATRACHIA; RANOIDEA; RANIDAE; RANINAE; RANA.
 RN [1]
 RA KOJIMA M.;
 RL SUBMITTED (XX-1992) TO EMBL/GENBANK/DBJ DATA BANKS.
 RP SEQUENCE FROM N.A.
 RX TISSUE-HEART;
 RT "Identification of new atrial natriuretic peptides in frog heart.";
 RL BIOCHEM. BIOPHYS. RES. COMMUN. 155:1338-1345(1988).
 CC -1- FUNCTION: VASOACTIVE ACTIVITY. HAS A CGMP-STIMULATING ACTIVITY.
 CC -1- SIMILARITY: BELONGS TO THE NATRIURETIC PEPTIDES FAMILY.
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 CC -----
 CC EMBL; D01043; D1001314; ..
 DR PIR: A31510; A31510.
 DR PIR: JQ0947; JQ0947.
 DR PROSITE; PS00263; NATRIURETIC_PEPTIDE; 1.
 DR PFAM; PF00212; ANP; 1.
 KW VASOACTIVE; SIGNAL.
 FT SIGNAL 1 23 POTENTIAL
 FT PEPTIDE 122 145 ATRIAL NATRIURETIC FACTOR.
 FT DISULFID 125 141
 SQ SEQUENCE 145 AA; 15934 MW; 6A1FA352 CRC32;
 Query Match 71.3%; Score 199; DB 1; Length 145;
 Best Local Similarity 71.1%; Pred. No. 4.13e-30;
 Matches 27; Conservative 5; Mismatches 4; Indels 2; Gaps 2;
 Db 109 LRELLNAPRSMRSDCFGSRIDRIGAQSGMCGGR-RF 145
 QY 1 LRALLAPRSLRSSCFGGRMDRIGAQSGLCNSFRY 37
 RESULT 11
 ID ANF_RANRI STANDARD; PRT: 30 AA.
 AC P09196;
 DT 01-MAR-1989 (REL. 10, CREATED)
 DT 01-MAR-1989 (REL. 10, LAST SEQUENCE UPDATE)
 DT 01-FEB-1995 (REL. 31, LAST ANNOTATION UPDATE)
 DE ATRIAL NATRIURETIC FACTOR (ANF) (ATRIAL NATRIURETIC PEPTIDE) (ANP).
 OS RANA RIDIBUNDA (LAUGHING FROG) (MARSH FROG).
 CC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; AMPHIBIA; BATRACHIA; ANURA;
 CC NEOBATRACHIA; RANOIDEA; RANIDAE; RANINAE; RANA.
 RN [1]
 RP SEQUENCE.
 RC TISSUE-HEART ATRIUM;
 RX MEDLINE; 89005705.
 RA LAZURE C., ONG H., MCNICOLL N., NETCHITAILO P., CHRETIEN M.,
 RA DE LEAN A., VAUDRY H.;
 RT "The amino acid sequences of frog heart atrial natriuretic-like
 peptide and mammalian ANF are closely related.";
 RL FEBS LETT. 238:300-306(1988).
 CC -1- FUNCTION: VASOACTIVE ACTIVITY. HAS A CGMP-STIMULATING ACTIVITY.
 CC -1- SIMILARITY: BELONGS TO THE NATRIURETIC PEPTIDES FAMILY.
 CC PIR: S01657; S01657.
 DR PROSITE; PS00263; NATRIURETIC_PEPTIDE; 1.
 DR PFAM; PF00212; ANP; 1.
 KW VASOACTIVE.
 FT DISULFID 11 27
 SQ SEQUENCE 30 AA; 3263 MW; 14A325F7 CRC32;
 Query Match 61.6%; Score 172; DB 1; Length 30;
 Best Local Similarity 76.7%; Pred. No. 3.12e-23;
 Matches 23; Conservative 4; Mismatches 2; Indels 1; Gaps 1;
 Db 1 APRSMRSDCFGSRIDRIGAQSGMCGGRF 30
 QY 7 APRSLRSSCFGGRMDRIGAQSGLCNSF 35
 RESULT 12
 ID ANFB_BOVIN STANDARD; PRT: 103 AA.
 AC P13204;
 DT 01-JAN-1990 (REL. 13, CREATED)
 DT 01-DEC-1992 (REL. 24, LAST SEQUENCE UPDATE)
 DT 01-OCT-1996 (REL. 34, LAST ANNOTATION UPDATE)
 DE BRAIN NATRIURETIC PEPTIDE PRECURSOR (BNP) (ALDOSTERONE SECRETION
 DE INHIBITORY FACTOR) (ASIF).
 GN NPPB.

```

RRL BIOCHEM. BIOPHYS. RES. COMMUN. 157:402-409(1988).
[4] SEQUENCE OF 100-131.
RRN MEDLINE; 88339957.
RX SUDOH T., MINAMINO N., KANGAWA K., MATSUO H.;
RA "Brain natriuretic peptide-32: N-terminal six amino acid extended
RRT form of brain natriuretic peptide identified in porcine brain.";
RRL BIOCHEM. BIOPHYS. RES. COMMUN. 155:726-732(1988).
[5]
RRN SEQUENCE OF 106-131.
RRP MEDLINE; 88156915.
RX SUDOH T., KANGAWA K., MINAMINO N., MATSUO H.;
RA "A new natriuretic peptide in porcine brain.";
RRT NATURE 332:78-81(1988).
RRL [6]
RRN STRUCTURE BY NMR OF BNP-26.
RRP MEDLINE; 91031435.
RX INOOKA H., KIUCHI T., ENDO S., ISHIBASHI Y., WAKIMASU M., MIZUTA E.;
RA "Conformation in solution of porcine brain natriuretic peptide
RRT determined by combined use of nuclear magnetic resonance and distance
RRT geometry.";
RRL EUR. J. BIOCHEM. 193:127-134(1990).
[7]
RRN STRUCTURE BY NMR OF BNP-26.
RRP MEDLINE; 92007873.
RX CRAIK D., MUNRO S., NIELSEN K., SHEHAN P., TREGEAR G., WADE J.;
RA "The conformation of porcine-brain natriuretic peptide by two-
RRT dimensional NMR spectroscopy.";
RRL EUR. J. BIOCHEM. 201:183-191(1991).
CC -!- FUNCTION: VASOACTIVE ACTIVITY.
CCC -!- TISSUE SPECIFICITY: BRAIN AND ALSO IN ATRIA, BUT AT MUCH LOWER
CCC LEVELS THAN ANP.
CCCC -!- SIMILARITY: BELONGS TO THE NATRIURETIC PEPTIDES FAMILY.
CCCC-----
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CCCC-----
EMBL; M23596; G535705; -.
DR EMBL; M25547; G164393; -.
DR PIR; A31675; A31675
DR PIR; A31676; A31676
DR PIR; A31517; A31517
DR PIR; A33873; A33873
DR PIR; S06359; S06359
DR PROSITE; PS00263; NATRIURETIC_PEPTIDE; 1.
DR PFAM; PF00212; ANP; 1.
KW VASOACTIVE; BRAIN; SIGNAL.
FT SIGNAL 1 25
FT CHAIN 26 131 GAMMA-BRAIN NATRIURETIC PEPTIDE.
FT PEPTIDE 100 131 BRAIN NATRIURETIC PEPTIDE (BNP-32).
FT FT PEPTIDE 106 131 BRAIN NATRIURETIC PEPTIDE (BNP-26).
FT DISULFID 109 125
FT VARIANT 26 26 H -> Y (IN A CLONE).
SQ SEQUENCE 131 AA; 14512 MW; 17699327 CRC32;

Query Match: 56.3% Score 157; DB 1; Length 131;
Best Local Similarity 55.3%; Pred. No. 1.65e+19;
Matches .21; Conservative 10; Mismatches 5; Indels 2; Gaps 2;

Db 95 LRGI-RSPKTMRDSCGFRRLDRIIGSLSGLCGNVLRRY 131
|::: |:::: |::| |::|:: |::|:: |::|:: |::
QY 1 LRALLPAPRSLLRSSCFGGRMDRIGAQSGLGCNSFR-Y 37

RESULT 14
ID ANFB_CANFA STANDARD; PRT; 140 AA.
AC F16859;
DT 01-AUG-1990 (REL. 15, CREATED)

```

Search completed: Wed Jun 16 12:50:07 1999
Job time : 21 secs.

WATERMANN
(TM)

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MPearch_pp protein - protein database search, using Smith-Waterman algorithm
Run on: Wed Jun 16 12:50:24 1999; MasPar time 6.96 Seconds
290.262 Million cell updates/sec
Tabular output not generated.

Title: >VANDER-027-213.PEP
Description: (1-37) from vander0277777.pep
Perfect Score: 279
Sequence: 1 LRALLTAPSLRRSCFCGRMDRIGAGSLGCSNFRY 37

Scoring table: PAM 150
Gap 11

Searched: 179066 seqs, 54579741 residues

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database: sptrenbl9
1:sp_archaea 2:sp_bacteria 3:sp_fungi 4:sp_human
5:sp_invertebrate 6:sp_mammal 7:sp_mhc 8:sp_organelle
9:sp_phase 10:sp_plant 11:sp_rodent 12:sp_unclassified
13:sp_vertebrate 14:sp_virus

Statistics: Mean 32.418; Variance 46.907; scale 0.691

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description	Pred. No.
1	279	100.0	151	4	Q13766	ATRIAL NATRIURETIC FAC
2	279	100.0	152	6	Q46540	ATRIAL NATRIURETIC PEP
3	272	97.5	155	6	Q29130	CARDIODILATIN, ATRIAL
4	152	54.5	129	6	Q46541	BRAIN NATRIURETIC PEP
5	106	38.0	121	11	O55086	BRAIN NATRIURETIC PEP
6	96	34.0	139	13	P79799	NATRIURETIC PEPTIDE
7	85	30.5	298	10	O82599	FL104.13 PROTEIN.
8	80	28.7	187	1	O29736	HYPOTHETICAL 21.2 KD P
9	78	28.0	334	1	O26948	GLUCOSAMINE--FRUCTOSE
10	77	27.6	2025	5	O62191	F31C3.3 PROTEIN.
11	74	26.5	461	11	O35947	NEUREGULIN.
12	74	26.5	1095	2	O55527	CHEMOTAXIS PROTEIN CHE
13	72	25.8	410	2	O52437	FERRDOXIN REDUCTASE.
14	72	25.8	2297	2	O54155	POLYKETIDE SYNTHASE.
15	71	25.4	232	1	O26659	CONSERVED PROTEIN.
16	71	25.4	419	14	O83025	UNKNOWN (FRAGMENT).
17	71	25.4	511	5	P90876	F46F3.2.
18	71	25.4	1186	5	Q17786	C07E3.3 PROTEIN.
19	71	25.4	2206	14	O83017	POLYPROTEIN 1A.
20	70	25.1	143	14	Q98255	MC088R.

21	70	25.1	179	4	O60597	IDURONATE-2-SULFATASE	1.97e+00
22	70	25.1	281	5	Q19208	COSMID F08F8	1.97e+00
23	70	25.1	343	4	Q14604	IDURONATE-2-SULPHATASE	1.97e+00
24	70	25.1	352	5	Q19209	COSMID F08F8	1.97e+00
25	70	25.1	390	8	Q33137	O-ACETYLSEIRINE-(THIOL)	1.97e+00
26	70	25.1	1810	5	Q18038	C16A3.2 PROTEIN	1.97e+00
27	70	25.1	1958	14	Q69340	ORF1, ORF2 AND ORF3	1.97e+00
28	69	24.7	192	10	O09236	PHYTOCHROME (FRAGMENT)	2.93e+00
29	69	24.7	442	13	P79878	RETINOIC ACID RECEPTOR	2.93e+00
30	69	24.7	601	4	Q43146	KIAA0396 (FRAGMENT)	2.93e+00
31	69	24.7	680	2	O52747	ENDO-GLUCANASE	2.93e+00
32	69	24.7	857	14	O83261	2A PROTEIN	2.93e+00
33	69	24.7	858	14	O65144	CMV-SD 2A	2.93e+00
34	69	24.7	1121	5	O01526	SIMILAR TO THE C. ELEG	2.93e+00
35	68	24.4	64	14	O83011	HYPOTHETICAL	4.32e+00
36	68	24.4	211	2	O66168	TRAI	4.32e+00
37	68	24.4	251	12	O54085	HYPOTHETICAL 28.0 KD P	4.32e+00
38	68	24.4	339	14	O65569	HYPOTHETICAL 36.0 KD P	4.32e+00
39	68	24.4	433	2	O06534	HYPOTHETICAL 46.0 KD P	4.32e+00
40	68	24.4	470	2	O51847	PHOSPHOMANNOMUTASE	4.32e+00
41	68	24.4	541	5	Q24197	ALPHA ESTERASE	4.32e+00
42	68	24.4	559	5	Q26645	ETS HOMOLOGUE	4.32e+00
43	67	24.0	45	14	Q64828	PVI PROTEIN (FRAGMENT)	6.35e+00
44	67	24.0	307	2	O52960	UNKNOWN PRODUCT	6.35e+00
45	67	24.0	414	4	Q13148	TAR DNA-BINDING PROTEI	6.35e+00

ALIGNMENTS

RESULT 1.
ID Q13766 PRELIMINARY: PRT; 151 AA.
AC Q13766;
DT 01-NOV-1996 (TREMBLREL. 01, CREATED)
DT 01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)
DT 01-JAN-1999 (TREMBLREL. 09, LAST ANNOTATION UPDATE)
DE ATRIAL NATRIURETIC FACTOR PRECURSOR.
OS HOMO SAPIENS (HUMAN).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA; PRIMATES;
RN CATARRHINI; HOMINIDAE; HOMO.
[1]
RP SEQUENCE FROM N.A.
RX MEDLINE: 85205210.
RA SEIDMAN C.E., BLOCH K.D., ZISFEIN J., SMIT J., HABER E., HOMCY C.,
RA DUBY A.D., CHOI E., GRAHAM R.M., SEIDMAN J.G.;
RT "Molecular studies of the atrial natriuretic factor gene."
RL HYPERTENSION 7:31-34(1985).
DR EMBL: M54947; G178638;
DR EMBL: M54951; G178638; JOINED.
DR PROSITE: P500263; NATRIURETIC_PEPTIDE; 1.
DR PFAM: PF00212; ANP; 1.
KW VASOACTIVE; SIGNAL.
FT SIGNAL 1 25
FT PEPTIDE 26 55 CARDIODILATIN-RELATED PEPTIDE (CDP).
FT PEPTIDE 134 151 ATRIAL NATRIURETIC PEPTIDE, ALPHA (ANP).
FT DISULFID 130 146 BY SIMILARITY.
SQ SEQUENCE 151 AA; 16381 MW; E8827DA3 CRC32;
Query Match 100.0%; Score 279; DB 4; Length 151;
Best Local Similarity 100.0%; Pred. No. 1.69e-50;
Matches 37; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Db 115 LRALLTAPSLRRSCFCGRMDRIGAGSLGCSNFRY 151
|||||
QY 1 LRALLTAPSLRRSCFCGRMDRIGAGSLGCSNFRY 37
RESULT 2
ID Q46540 PRELIMINARY: PRT; 152 AA.
AC Q46540;
DT 01-JUN-1998 (TREMBLREL. 06, CREATED)
DT 01-JUN-1998 (TREMBLREL. 06, LAST SEQUENCE UPDATE)
DT 01-AUG-1998 (TREMBLREL. 07, LAST ANNOTATION UPDATE)
DE ATRIAL NATRIURETIC PEPTIDE.

GN ANP.
 OS OVIS ARIES (SHEEP).
 OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA;
 OC ARTIODACTYLIA; RUMINANTIA; PECORA; BOVIDAE; BOVINAE; CAPRINAE; OVIS.
 RN [1]
 RP SEQUENCE FROM N.A.
 RA AITKEN G.D., RAIKIS A.M., GEORGE P.M., ESPINER E.A., CAMERON V.A.;
 RL SUBMITTED (DEC-1997) TO EMBL/GENBANK/DBJ DATA BANKS.
 DR EMBL: AF037465; G2708650;
 DR PROSITE: PS00263; NATRIURETIC_PEPTIDE; 1.
 SQ SEQUENCE 152 AA; 16368 MW; D5360BCC CRC32;

Query Match 100.0%; Score 279; DB 6; Length 152;
 Best Local Similarity 100.0%; Pred. No. 1.69e-50;
 Matches 37; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 114 LRALLTAPRLSRSSCFGRMDRIGAGSLGNCNSFR 150
 QY 1 LRALLTAPRLSRSSCFGRMDRIGAGSLGNCNSFR 37

RESULT 3
 ID Q29130 PRELIMINARY; PRT: 155 AA.
 AC Q29130;
 DT 01-NOV-1996 (TREMELREL. 01, CREATED)
 DT 01-NOV-1996 (TREMELREL. 01, LAST SEQUENCE UPDATE)
 DT 01-NOV-1998 (TREMELREL. 08, LAST ANNOTATION UPDATE)
 DE CARDIOLATIN, ATRIAL NATRIURETIC PEPTIDE.
 OS TUPAIA BELANGERI.
 OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA;
 OC SCANDENTIA; TUPAIIDAE; TUPAIA.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=HEART;
 RA SCHNEIDEMANN S., MAEGERT H.J., FORSSMANN W.G.;
 RL SUBMITTED (MAR-1996) TO EMBL/GENBANK/DBJ DATA BANKS.
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=HEART;
 RA PARIGOL A.;
 RL SUBMITTED (MAR-1996) TO EMBL/GENBANK/DBJ DATA BANKS.
 DR EMBL: 270294; E233859;
 DR PROSITE: PS00263; NATRIURETIC_PEPTIDE; 1.
 DR PFAM: PF00212; ANP; 1.
 SQ SEQUENCE 155 AA; 16860 MW; 7758CA8B CRC32;

Query Match 97.5%; Score 272; DB 6; Length 155;
 Best Local Similarity 94.6%; Pred. No. 1.24e-48;
 Matches 35; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Db 117 LRALLTAPRLSRSSCFGRMDRIGAGSLGNCNSFR 153
 QY 1 LRALLTAPRLSRSSCFGRMDRIGAGSLGNCNSFR 37

RESULT 4
 ID O46541 PRELIMINARY; PRT: 129 AA.
 AC O46541;
 DT 01-JUN-1998 (TREMELREL. 06, CREATED)
 DT 01-JUN-1998 (TREMELREL. 06, LAST SEQUENCE UPDATE)
 DT 01-AUG-1998 (TREMELREL. 07, LAST ANNOTATION UPDATE)
 DE BRAIN NATRIURETIC PEPTIDE.
 GN BNP.
 OS OVIS ARIES (SHEEP).
 OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA;
 OC ARTIODACTYLIA; RUMINANTIA; PECORA; BOVIDAE; BOVINAE; CAPRINAE; OVIS.
 RN [1]
 RP SEQUENCE FROM N.A.
 RA AITKEN G.D., RAIKIS A.M., GEORGE P.M., ESPINER E.A., CAMERON V.A.;
 RL SUBMITTED (DEC-1997) TO EMBL/GENBANK/DBJ DATA BANKS.
 DR EMBL: AF037466; G2708652;
 DR PROSITE: PS00263; NATRIURETIC_PEPTIDE; 1.
 SQ SEQUENCE 129 AA; 14118 MW; 85DE4222 CRC32;

Query Match 54.5%; Score 152; DB 6; Length 129;
 Best Local Similarity 57.9%; Pred. No. 5.58e-18;
 Matches 22; Conservative 8; Mismatches 6; Indels 2; Gaps 2;

Db 93 LRALLTAPRLSRSSCFGRMDRIGAGSLGNCNSFR 129
 QY 1 LRALLTAPRLSRSSCFGRMDRIGAGSLGNCNSFR 37

RESULT 5
 ID O5086 PRELIMINARY; PRT: 121 AA.
 AC O5086;
 DT 01-JUN-1998 (TREMELREL. 06, CREATED)
 DT 01-JUN-1998 (TREMELREL. 06, LAST SEQUENCE UPDATE)
 DT 01-NOV-1998 (TREMELREL. 08, LAST ANNOTATION UPDATE)
 DE BRAIN NATRIURETIC PEPTIDE.
 GN BNP.
 OS MUS MUSCULUS (MOUSE).
 OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA; RODENTIA;
 OC SCIUROGNATHI; MURIDAE; MURINAE; MUS.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=129/SV;
 RX MEDLINE: 94237953;
 RA OGAWA Y., ITOH H., TAMURA N., SUGA S., YOSHIMASA T., UEHIRA M.,
 RA MATSUDA S., SHIONO S., NISHIMOTO H., NAKAO K.;
 RT "Molecular cloning of the complementary DNA and gene that encode mouse brain natriuretic peptide and generation of transgenic mice that overexpress the brain natriuretic peptide gene.";
 RL J. CLIN. INVEST. 93:1911-1921(1994).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=129/SV;
 RX MEDLINE: 97031884;
 RA TAMURA N., OGAWA Y., YASODA A., NAKAO K.;
 RT "Two cardiac natriuretic peptide genes (atrial natriuretic peptide and brain natriuretic peptide) are organized in tandem in the mouse and human genomes.";
 RL J. MOL. CELL. CARDIOL. 28:1811-1815(1996).
 DR EMBL: D82049; D1025069;
 DR PROSITE: PS00263; NATRIURETIC_PEPTIDE; 1.
 SQ SEQUENCE 121 AA; 13730 MW; E3BFEC0B CRC32;

Query Match 38.0%; Score 106; DB 11; Length 121;
 Best Local Similarity 60.9%; Pred. No. 1.79e-07;
 Matches 14; Conservative 6; Mismatches 3; Indels 0; Gaps 0;

Db 97 SSCFGKHIDRIGSVSRIGCNALK 119
 QY 14 SSCFGKHIDRIGSVSRIGCNALK 36

RESULT 6
 ID P79799 PRELIMINARY; PRT: 139 AA.
 AC P79799;
 DT 01-MAY-1997 (TREMELREL. 03, CREATED)
 DT 01-MAY-1997 (TREMELREL. 03, LAST SEQUENCE UPDATE)
 DT 01-NOV-1998 (TREMELREL. 08, LAST ANNOTATION UPDATE)
 DE NATRIURETIC PEPTIDE.
 OS MICRURUS CORALLINUS.
 OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; LEPIDOSAURIA; SQUAMATA;
 OC SCLEROGLOSSA; SERPENTES; COLUBROIDEA; ELAPIDAE; MICRURUS.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=VENOM GLAND;
 RA HO P.L., SOARES M.B., YAMANE T., RAW I.;
 RL J. TOXICOL. TOXIN. REV. 14:327-337(1995).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=VENOM GLAND;
 RX MEDLINE: 9809229;
 RA HO P.L., SOARES M.B., MAACK T., GIMENEZ I., PUERTO G., FURTADO M.F.D.,

RA RAW I.;
 RT *Cloning of an unusual natriuretic peptide from the South American
 RL coral snake *Micrurus corallinus*.;
 RL EUR. J. BIOCHEM. 250:144-149(1997).
 DR EMBL; U77596; G1684874;
 DR PROSITE; PS00263; NATRIURETIC_PEPTIDE; 1.
 DR PFAM; PF00212; ANP; 1.
 SQ SEQUENCE 139 AA; 14881 MW; 05421ABB CRC32;

Query Match 34.4%; Score 96; DB 13; Length 139;
 Best Local Similarity 59.1%; Pred. No. 2.24e-05;
 Matches 13; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

Db 85 GCGGDRICNVSGMGNHYR 106
 Qy 15 SCFGGMDRIGAQSGLGCNSFR 36

RESULT 7
 ID O82599 PRELIMINARY; PRT; 298 AA.
 AC O82599;
 DT 01-NOV-1998 (TREMBLREL. 08, CREATED)
 DT 01-NOV-1998 (TREMBLREL. 08, LAST SEQUENCE UPDATE)
 DT 01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)
 DE F1104.13 PROTEIN.
 GN F1104.13.
 OS ARABIDOPSIS THALIANA (MOUSE-EAR CRESS).
 OC EUKARYOTA; VIRIDIPANTAE; STREPTOPHYTA;
 OC EUPHYLLOPHYTES; SPERMATOPHYTA; MAGNOLIOPHYTA; EUDICOTYLEDONS; ROSIDAE;
 OC CAPPARALES; BRASSICACEAE; ARABIDOPSIS.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-CV. COLUMBIA;
 RA WASHU;
 RT *The A. thaliana Genome Sequencing Project.*;
 RL SUBMITTED (OCT-1998) TO EMBL/GENBANK/DBJ DATA BANKS.
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN-CV. COLUMBIA;
 RA ABU-THREIDEH J.; STONEKING T.; LANGSTON Y.; TREVASKIS E.;
 RT "The sequence of A. thaliana F1104.";
 RL SUBMITTED (OCT-1998) TO EMBL/GENBANK/DBJ DATA BANKS.
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN-CV. COLUMBIA;
 RA WATERSTON R.;
 RL SUBMITTED (OCT-1998) TO EMBL/GENBANK/DBJ DATA BANKS.
 DR EMBL; AF096370; G3695384;
 SQ SEQUENCE 298 AA; 33450 MW; 61E11354 CRC32;

Query Match 30.5%; Score 85; DB 10; Length 298;
 Best Local Similarity 35.5%; Pred. No. 3.52e-03;
 Matches 11; Conservative 11; Mismatches 7; Indels 2; Gaps 2;

Db 135 LRSML-PPSFLORVTKCFKGLKNGKQDQSI 164
 Qy 1 LRALLTAPRSLRR-SSCFGMDRIGAQSGL 30

RESULT 8
 ID O29736 PRELIMINARY; PRT; 187 AA.
 AC O29736;
 DT 01-JAN-1998 (TREMBLREL. 05, CREATED)
 DT 01-JAN-1998 (TREMBLREL. 05, LAST SEQUENCE UPDATE)
 DT 01-AUG-1998 (TREMBLREL. 07, LAST ANNOTATION UPDATE)
 DE HYPOTHETICAL 21.2 KD PROTEIN.
 GN AF0514.
 OS ARCHAEOLLOBUS FULGIDUS.
 OC ARCHAEA; EURYARCHAEOTA; ARCHAEOLLOBALES; ARCHAEOLLOBACEAE;
 OC ARCHAEOLLOBUS.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-VC-16 / DSM 4304 / ATCC 49558;

RX MEDLINE; 98049343.
 RA KLENK H.-P., CLAYTON R.A., TOMB J.-F., WHITE O., NELSON K.E.,
 RA KETCHUM K.A., DODSON R.J., GWINN M., HICKEY E.K., PETERSON J.D.,
 RA RICHARDSON D.L., KERLAVAGE A.R., GRAHAM D.E., KIRPIDES N.C.,
 RA FLEISCHMANN R.D., DOUGHERTY B.A., MCKENNEY K., SUTTON G.G., GILL S.,
 RA KIRKNESS E.F., DOUGHERTY B.A., MCKENNEY K., ADAMS M.D., LOFTUS B.,
 RA PETERSON S., REICH C.I., MCNEIL L.K., BADGER J.H., GLODER A., ZHOU L.,
 RA OVERBEER R., GOCAYNE J.D., WEIDMAN J.F., MCDONALD L., UTTERBACK T.,
 RA COTTON M.D., SPRIGGS T., ARTIACH P., KATNE B.P., SYKES S.M.,
 RA SADOW P.W., D'ANDREA K.P., BOWMAN C., FUJII C., GARLAND S.A.,
 RA MASON T.M., OLSEN G.J., FRASER C.M., SMITH H.O., WOESSE C.R.,
 RA VENTER J.C.;
 RT "The complete genome sequence of the hyperthermophilic,
 RT sulphate-reducing archaeon *Archaeoglobus fulgidus*.";
 RL NATURE 390:364-370(1997).
 DR EMBL; AE001058; G2650115;
 DR TIGR; AF0514;
 KW HYPOTHETICAL PROTEIN.
 SQ SEQUENCE 187 AA; 21243 MW; D7BE7C22 CRC32;

Query Match 28.7%; Score 80; DB 1; Length 187;
 Best Local Similarity 44.0%; Pred. No. 3.15e-02;
 Matches 11; Conservative 8; Mismatches 6; Indels 0; Gaps 0;

Db 21 ALLCPHPLMGSGRFVRLERIAAE 45
 Qy 3 ALLTAPRSLRRSSCFGMDRIGAQ 27

RESULT 9
 ID O26948 PRELIMINARY; PRT; 334 AA.
 AC O26948;
 DT 01-JAN-1998 (TREMBLREL. 05, CREATED)
 DT 01-JAN-1998 (TREMBLREL. 05, LAST SEQUENCE UPDATE)
 DT 01-AUG-1998 (TREMBLREL. 07, LAST ANNOTATION UPDATE)
 DE GLUCOSAMINE--FRUCTOSE-6-PHOSPHATE AMINOTRANSFERASE.
 GN MTH860.
 OS METHANOBACTERIUM THERMOAUTOTROPHICUM.
 OC ARCHAEA; EURYARCHAEOTA; METHANOBACTERIALES; METHANOBACTERIACEAE;
 OC METHANOBACTERIUM.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-DELTA H;
 RX MEDLINE; 98037514.
 RA SMITH D.R., DOUCETTE-STAMM L.A., DELOUGHERY C., LEE H.-M., DUBOIS J.,
 RA ALDRIDGE T., BASHIRZADEH R., BLAKELY D., COOK R., GILBERT K.,
 RA HARRISON D., HOANG L., KEAGLE P., LUMM W., POTHIER B., QIU D.,
 RA SPADAFORA R., VICARE R., WANG Y., WIERZBOWSKI J., GIBSON R.,
 RA JIWANI N., CARUSO A., BUSH D., SAFER H., PATWELL D., PRABHAKAR S.,
 RA MCDUGALL S., SHIMER G., GOYAL A., PIETROVSKI S., CHURCH G.M.,
 RA DANIELS C.J., MAO J.-I., RICE P., NOLLING J., REEVE J.N.;
 RT "Complete genome sequence of *Methanobacterium thermoautotrophicum*
 RT delta: functional analysis and comparative genomics.";
 RL J. BACTERIOL. 179:7135-7155(1997).
 DR EMBL; AE000862; G2621952;
 KW TRANSFERASE; AMINOTRANSFERASE.
 SQ SEQUENCE 334 AA; 37853 MW; B5B5BA4C CRC32;

Query Match 28.0%; Score 78; DB 1; Length 334;
 Best Local Similarity 43.3%; Pred. No. 7.40e-02;
 Matches 13; Conservative 4; Mismatches 11; Indels 2; Gaps 2;

Db 9 LMEQESLRRLTKSEGDMARISNEI-LEC 37
 Qy 4 LLTAPRSLRRS-SCFGGMDRIGAQSGLGC 32

RESULT 10
 ID O62191 PRELIMINARY; PRT; 2025 AA.
 AC O62191;
 DT 01-AUG-1998 (TREMBLREL. 07, CREATED)
 DT 01-AUG-1998 (TREMBLREL. 07, LAST SEQUENCE UPDATE)
 DT 01-JAN-1999 (TREMBLREL. 09, LAST ANNOTATION UPDATE)

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DE F31C3.3 PROTEIN.
GN F31C3.3.
OS CAENORHABDITIS ELEGANS.
OC EUKARYOTA; METAZOA; NEMATODA; SECERNENTEA; RHABDITIA; RHABDITIDA;
OC RHABDITINA; RHABDITOIDEA; RHABDITIDAE; PELODERINAE; CAENORHABDITIS.
RN [1]
RP SEQUENCE FROM N.A.
RC COTTAGE A.;
RA SUBMITTED (MAR-1997) TO EMBL/GENBANK/DBJ DATA BANKS.
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE; 94150718.
RA WILSON R., AINSOUGH R., ANDERSON K., BAYNES C., BERKS M.,
RA BONFIELD J., BURTON J., CONNELL M., COPSEY T., COOPER J., COULSON A.,
RA CRAXTON M., DEAR S., DU Z., DURBIN R., FAVELLO A., FULTON L.,
RA GARDNER A., GREEN P., HAWKINS T., HILLIER L., JIER M., JOHNSTON L.,
RA JONES M., KERSHAW J., KIRSTEN J., LAISTER N., LATREILLE P.,
RA LIGHTNING J., LLOYD C., MCMURRAY A., MORTIMORE B., O'CALLAGHAN M.,
RA PARSONS J., PERCY C., RIFKEN L., ROOPRA A., SAUNDERS D., SHOWNKEEN R.,
RA SNALDON N., SMITH A., SONNHAMMER E., STADEN R., SULSTON J.,
RA THIERRY-NIEG J., THOMAS K., VAUDIN M., VAUGHAN K., WATERSTON R.,
RA WATSON A., WEINSTOCK L., WILKINSON-SPROAT J., WOHLDMAN P.;
RT "2.2 Mb of contiguous nucleotide sequence from chromosome III of C.
RL NATURE 368:32-38(1994).
DR EMBL; Z92784; E1346409.
SQ SEQUENCE 2025 AA; 234375 MW; CF2EB634 CRC32;

Query Match 27.6%; Score 77; DB 5; Length 2025;
Best Local Similarity 42.9%; Pred. No. 1.13e-01;
Matches 9; Conservative 7; Mismatches 5; Indels 0; Gaps 0;

Db 1127 LKSLTKNNVRRCVTGCVNRV 1147
      ||||| |::||::||| |
QY 1 LRALLTAPRSLRSSCFGRM 21

RESULT 11
ID Q35947 PRELIMINARY; PRT; 461 AA.
AC Q35947;
DT 01-JAN-1998 (TREMBLREL. 05, CREATED)
DT 01-JAN-1998 (TREMBLREL. 05, LAST SEQUENCE UPDATE)
DT 01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)
DE NEUREGULIN.
OS MESOCRICETUS AURATUS (GOLDEN HAMSTER).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA; RODENTIA;
OC SCIUROGNATHI; MORIDAE; CRICETINAE; MESOCRICETUS.
RN [1]
RP SEQUENCE FROM N.A.
RA VELASCO J.A., FEIJOO E., AVILA M.A., NOTARIO V.;
RL SUBMITTED (APR-1997) TO EMBL/GENBANK/DBJ DATA BANKS.
DR EMBL; U96612; G2459765.
DR PROSITE; PS01186; EGF_2; 1.
DR PFAM; PF00008; EGF; 1.
DR PFAM; PF00047; 19; 1.
KW GLYCOPROTEIN.
SQ SEQUENCE 461 AA; 50890 MW; E937DA34 CRC32;

Query Match 26.5%; Score 74; DB 11; Length 461;
Best Local Similarity 37.5%; Pred. No. 3.93e-01;
Matches 12; Conservative 9; Mismatches 11; Indels 0; Gaps 0;

Db 372 MNSSVENSRRHSSPAGPGRHLHGLGLOCNSF 403
      :::: :|::||| |
QY 4 LITAPRSLRSSCFGRMDRIGAOGLGNCNSF 35

RESULT 12
ID Q55527 PRELIMINARY; PRT; 1095 AA.
AC Q55527;
DT 01-NOV-1996 (TREMBLREL. 01, CREATED)
DT 01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)
DT 01-JAN-1999 (TREMBLREL. 09, LAST ANNOTATION UPDATE)

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DE CHEMOTAXIS PROTEIN CHEA.
GN CHEA.
OS SYNECHOCYSTIS SP. (STRAIN PCC 6803).
OC BACTERIA; CYANOBACTERIA; CHROCOCCALES; SYNECHOCYSTIS.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-PCC6803;
RA TABATA S.;
RL SUBMITTED (AUG-1995) TO EMBL/GENBANK/DBJ DATA BANKS.
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE; 96127529.
RA KANEKO T., TANAKA A., SATO S., KOTANI H., SAZUKA T., MIYAJIMA N.,
RA SUGIURA M., TABATA S.;
RT "Sequence analysis of the genome of the unicellular cyanobacterium
RT Synechocystis sp. strain PCC6803. I. sequence features in the lmb
RT region from map positions 64 to 92 of the genome.";
RL DNA RES. 2:153-166(1995).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN-PCC6803;
RX MEDLINE; 97061201.
RA KANEKO T., SATO S., KOTANI H., TANAKA A., ASAMIZU E., NAKAMURA Y.,
RA MIYAJIMA N., HIROSAWA M., SUGIURA M., SASAMOTO S., KIMURA T.,
RA HOSOUCHI T., MATSUNO A., MURAKI A., NAKAZAKI N., NARUO K., OKUMURA S.,
RA SHIMO S., TAKEUCHI C., WADA T., WATANABE A., YAMADA M., YASUDA M.,
RA TABATA S.;
RT "Sequence analysis of the genome of the unicellular cyanobacterium
RT Synechocystis sp. PCC6803. II. Sequence determination of the entire
RT genome and assignment of potential protein-coding regions.";
RL DNA RES. 3:109-136(1996).
DR EMBL; D63999; D1010673; -.
DR PFAM; PF00072; response.reg; 2.
DR PFAM; PF00512; signal; 1.
SQ SEQUENCE 1095 AA; 120557 MW; 6697EB16 CRC32;

Query Match 26.5%; Score 74; DB 2; Length 1095;
Best Local Similarity 40.9%; Pred. No. 3.93e-01;
Matches 9; Conservative 5; Mismatches 8; Indels 0; Gaps 0;

Db 682 LKDLNLYNRLSRGVSIVGKOE 703
      ||| | | | | | | |
QY 1 LRALLTAPRSLRSSCFGRMD 22

RESULT 13
ID Q52437 PRELIMINARY; PRT; 410 AA.
AC Q52437;
DT 01-NOV-1996 (TREMBLREL. 01, CREATED)
DT 01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)
DT 01-JAN-1999 (TREMBLREL. 09, LAST ANNOTATION UPDATE)
DE FERREDOXIN REDUCTASE.
GN BPH4.
OS PSEUDOMONAS SP.
OC BACTERIA; PROTEOBACTERIA.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-KKS102;
RX MEDLINE; 94179104.
RA KIKUCHI Y., NAGATA Y., HINATA M., KIMBARA K., FUKUDA M., YANO K.,
RA TAKAGI M.;
RT "Identification of the bphA4 gene encoding ferredoxin reductase
RT involved in biphenyl and polychlorinated biphenyl degradation in
RT Pseudomonas sp. strain KKS102.";
RL J. BACTERIOL. 176:1689-1694(1994).
DR EMBL; D16831; D1004633; -.
SQ SEQUENCE 410 AA; 44101 MW; AE4622D0 CRC32;

Query Match 25.8%; Score 72; DB 2; Length 410;
Best Local Similarity 33.8%; Pred. No. 8.88e-01;
Matches 10; Conservative 10; Mismatches 10; Indels 0; Gaps 0;

```


RESULT	15	
ID	O26659	PRELIMINARY; PRT; 232 AA.
AC	O26659;	
DT	01-JAN-1998	(TREMBLEL. 05, CREATED)
DD	01-JAN-1998	(TREMBLEL. 05, LAST SEQUENCE UPDATE)
DT	01-AUG-1998	(TREMBLEL. 07, LAST ANNOTATION UPDATE)
DZ		CONSERVED PROTEIN.
GN	MTH559.	
OS	METHANOBACTERIUM THERMOAUTOTROPHICUM.	
OC	ARCHAEA; EURYARCHAEOTA; METHANOBACTERIALES; METHANOBACTERIACEAE;	
ON	METHANOBACTERIUM.	
KC	[1]	
RP	SEQUENCE FROM N.A.	
RC	STRAIN-DELTA H;	
RX	MEDLINE; 98037514.	
RA	SAMITH D.R., DOUCETTE-STAMM L.A., DELOUGHERY C., LEE H.-M., DUBOIS J.J.	
RA	ALDREGE T., BASHIRZADEH R., BLAKELY D., COOK R., GILBERT K.,	
RA	HARRISON D., HOANG L., KEAGLE P., LUMM W.S., POTIER B., QIU D.,	
RA	SPADAFORA R., VICARE R., WANG Y., WIERZBOWSKI J., GIBSON R.,	
RA	JIWANI N., CARUSO A., BUSH D., SAFER H., PATWELL D., PRABHAKAR S.,	
RA	MCDOUGALL S., SHIMER G., GOYAL A., PIETROWSKI S., CHURCH G.M.,	
RA	DANIELS C.J., MAO J.-I., RICE P., NOLLING J., REVEE J.N.;	
RT	*complete genome sequence of Methanobacterium thermoautotrophicum	
RT	deltah: functional analysis and comparative genomics.*	